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PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a **PROVISIONAL APPLICATION FOR PATENT** under 37 CFR 1.53 (c).

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TITLE OF THE INVENTION (500 characters max)

POLYPEPTIDES FOR INDUCING A PROTECTIVE IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

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Respectfully submitted,

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EXPRESS MAIL CERTIFICATE

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TITLE OF THE INVENTION
POLYPEPTIDES FOR INDUCING A PROTECTIVE IMMUNE RESPONSE
AGAINST *STAPHYLOCOCCUS AUREUS*

5   BACKGROUND OF THE INVENTION

The references cited throughout the present application are not
admitted to be prior art to the claimed invention.

Staphylococcus aureus is a pathogen responsible for a wide range of
diseases and conditions. Examples of diseases and conditions caused by *S. aureus*
10   include bacteremia, infective endocarditis, folliculitis, furuncle, carbuncle, impetigo,
bullous impetigo, cellulitis, botryomyosis, toxic shock syndrome, scalded skin
syndrome, central nervous system infections, infective and inflammatory eye disease,
osteomyletitis and other infections of joints and bones, and respiratory tract
infections. (*The Staphylococci in Human Disease*, Crossley and Archer (eds.),
15   Churchill Livingstone Inc. 1997.)

Immunological based strategies can be employed to control *S. aureus*
infections and the spread of *S. aureus*. Immunological based strategies include
passive and active immunization. Passive immunization employs immunoglobulins
targeting *S. aureus*. Active immunization induces immune responses against *S.*
20   *aureus*.

Potential *S. aureus* vaccines target *S. aureus* polysaccharides and
polypeptides. Targeting can be achieved using *S. aureus* polysaccharides or
polypeptides as vaccine components. Examples of polysaccharides that may be
employed as possible vaccine components include *S. aureus* type 5 and type 8
25   capsular polysaccharides. (*Shinefield et al., N. Eng. J. Med. 346*:491-496, 2002.)
Examples of polypeptides that may be employed as possible vaccine components
include collagen adhesin, fibrinogen binding proteins, and clumping factor. (Mamo
et al., FEMS Immunology and Medical Microbiology 10:47-54, 1994, Nilsson *et al.,*
J. Clin. Invest. 101:2640-2649, 1998, Josefsson *et al., The Journal of Infectious*
30   *Diseases 184*:1572-1580, 2001.)

Information concerning *S. aureus* polypeptide sequences has been
obtained from sequencing the *S. aureus* genome. (Kuroda *et al., Lancet 357*:1225-
1240, 2001, Baba *et al., Lancet 359*:1819-1827, 2000, Kunsch *et al.,* European Patent
Publication EP 0 786 519, published July 30, 1997.) To some extent bioinformatics
35   has been employed in efforts to characterize polypeptide sequences obtained from

genome sequencing. (Kunsch *et al.*, European Patent Publication EP 0 786 519, published July 30, 1997.)

Techniques such as those involving phage display technology and sera from infected patients can be used in an effort to identify genes coding for potential

5   antigens. (Foster *et al.*, International Publication Number WO 01/98499, published December 27, 2001.)

SUMMARY OF THE INVENTION

The present invention features hybrid polypeptides providing

10   ORF0657n and ORFO190 epitopes, ORF0657n polypeptides, nucleic acid encoding for the different polypeptides, and a method for evaluating the ability of an immunogen to produce a protective immune response against *Staphylococcus* infection. ORF0657n and ORF0190 are both *S. aureus* proteins.

A preferred use of hybrid and ORF0657n polypeptides is to induce a

15   protective immune response against *S. aureus*. Protective immunity or immune response provides a detectable level of protection against *S. aureus* infection. The level of protection can be assessed using animal models such as those described in Example 1 *infra*.

Thus, a first aspect of the present invention describes a hybrid

20   polypeptide comprising a modified ORF0657n sequence segment at least about 100 amino acids in length. An ORF0657n "sequence segment" provides all or a portion of an ORF0657n protein as a references sequence.

Hybrid polypeptides comprise a modified ORF0657n sequence segment containing one or more alterations increasing sequence similarity to SEQ ID

25   NO: 1 (ORF0190). The modified ORF0657n sequence segment comprises one or more alterations increasing sequence similarity to SEQ ID NO: 1. An amino acid alteration is an addition, deletion, or substitution. Different combinations of amino acids alterations may be present.

Reference to an alteration or modification is a structural distinction

30   between a reference sequence and is not a method of production limitation. Altered and modified sequences can be produced, for example, by altering a preexisting sequence or synthesizing a desired sequence.

Reference to "polypeptide" includes salt forms and does not provide a size limitation or function. A polypeptide may include, for example, a protein or a

35   fragment thereof.

Another aspect of the present invention features a method of making a
hybrid polypeptide comprising a modified ORF0657n sequence. The method
comprises the step of introducing one or more alterations into a ORF0657n sequence
segment at least about 100 amino acids in length, wherein at least one of the
5   alterations increases sequence similarity to SEQ ID NO: 1.

Another aspect of the present invention describes an isolated
ORF0657n polypeptide comprising an amino acid sequence selected from the group
consisting of SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, and
SEQ ID NO: 7. An isolated polypeptide is a polypeptide that is present in a different
10   form than found in nature. The different form may be, for example, a purified form.

Another aspect of the present invention describes a mutated
ORF0657n polypeptide comprising amino acids 2-646 of SEQ ID NO: 44. In
different embodiments the polypeptide consists of an amino acid sequence starting at
either amino acid 1 or 2 of SED ID NO: 44 and ending at an amino acid from 646-654
15   of SEQ ID NO: 44. In preferred embodiments the polypeptide consists of amino
acids 1-646 or 2-646 of SEQ ID NO: 44.

Preferably, the mutated ORF0657n polypeptide is substantially pure.
Reference to a substantially pure polypeptide indicates that polypeptide is at least
about 80% of the protein present in a sample. In different embodiment the
20   substantially pure polypeptide provides at least 85%, at least 95%, or at least 99% of
the protein present in a sample.

Another aspect of the present invention features an immunogen
comprising a polypeptide that induces protective immunity against S. aureus. The
immunogen comprises a polypeptide described herein.

25   Reference to "immunogen" indicates the ability to produce an immune
response. An immunogen contains one or more polypeptide regions, and may also
contain one or more regions that are not polypeptides and/or one or more moieties
that are not amino acids.

Another aspect of the present invention describes a composition able
30   to induce a protective immune response in a patient. The composition comprises an
immunologically effective amount of an immunogen that induces protective
immunity against S. aureus and a pharmaceutically acceptable carrier.

An immunologically effective amount is an amount sufficient to
provide protective immunity against S. aureus infection. The amount should be
35   sufficient to significantly prevent the likelihood or severity of a S. aureus infection.

3

Another aspect of the present invention describes a method of inducing a protective immune response in a patient against *S. aureus*. The method comprises the step of administering to the patient an immunologically effective amount of an immunogen.

5   Another aspect of the present invention describes a nucleic acid comprising a nucleotide sequence encoding a polypeptide described herein. In a preferred embodiment the nucleic acid is a recombinant nucleic acid. Recombinant nucleic acid is nucleic acid that by virtue of its sequence or form does not occur in nature.

10   Another aspect of the present invention describes a cell comprising a recombinant gene encoding a polypeptide described herein. A recombinant gene contains recombinant nucleic acid encoding a polypeptide along with regulatory elements for proper transcription and processing.

Another aspect of the present invention describes a method for

15   evaluating the efficacy of an immunogen to produce a protective immune response against *Staphylococcus*. The method comprises the steps of:

(a) immunizing an animal model with an immunogen;

(b) challenging the immunized animal model with a *Staphylococcus* challenge at a potency that provides about 80 to 90% death in an non-immunized

20   animal model over a period of about 7-10 days starting on the first or second day, wherein the *Staphylococcus* challenge is produced from *Staphylococcus* grown to stationary phase, and the *Staphylococcus* challenge is intravenously introduced into the animal; and

(c) measuring the ability of the immunogen to provide protective

25   immunity.

Reference to "animal model" excludes humans. Suitable animal models are non-human mammals able to mount an immune defensive against *S. aureus*. Examples of animal models include mice, rats, primates and cattle.

Unless particular terms are mutually exclusive, reference to "or"

30   indicates either or both possibilities. Occasionally phrases such as "and/or" are used to highlight either or both possibilities.

Other features and advantages of the present invention are apparent from the additional descriptions provided herein including the different examples. The provided examples illustrate different components and methodology useful in

35   practicing the present invention. The examples do not limit the claimed invention.

Based on the present disclosure the skilled artisan can identify and employ other components and methodology useful for practicing the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

5   Figures 1A, 1B and 1C illustrate a sequence comparison between ORF0190 (SEQ ID NO: 1), 0657n (SEQ ID NO: 2), 0657nHybrid1 (SEQ ID NO: 8), 0657nHybrid2 (SEQ ID NO: 9), and 0657nHybrid3 (SEQ ID NO: 10). SEQ ID NOs: 8, 9 and 10 are examples of hybrid polypeptides comprising a modified ORF0657n sequence segment.

10   Figures 2A-2L provide examples of different hybrid sequences (SEQ ID NOs: 8-43).

Figure 3 illustrates forward and reverse PCR primer sequences for amplifying a nucleic acid sequence to encode a mutated form of ORF 0657n. ORF 0657n amino acids are indicated in non italics; added amino acids (the initiator M and

15   G) coded by the forward primer are indicated by italics. Restriction sites are underlined. Non-expressed regions are in parenthesis. SEQ ID NOs: 46 and 48 are forward and reverse primer sequences. SEQ ID NOs: 47 and 49 are the amino acid sequences encoded by the forward and reverse primers.

Figures 4A and 4B illustrate translation of a cloned and expressed

20   mutated form of ORF 0657n. The mutated form of ORF 0657n contains modifications to facilitate cloning and purification. Figure 4A illustrates the expressed sequence including additional histidine residues (SEQ ID NO: 44). Figure 4B illustrates an abbreviated alignment of the native and mutated forms of ORF 0657n showing differences between the two forms.

25   Figure 5 illustrates survival data using a mutated ORF 0657n in aluminum hydroxyphosphate adjuvant (AHP).

DETAILED DESCRIPTION OF THE INVENTION

The present invention features a hybrid polypeptide comprising a

30   modified ORF0657n sequence segment, different ORF0657n polypeptides, nucleic acid encoding such polypeptides and a method for evaluating the ability of an immunogen to produce a protective immune response against *Staphylococcus* infection. Hybrid polypeptides and different ORF0657n polypeptides have therapeutic and diagnostic applications, such as being used to provide protective

35   immunity against a *S. aureus* infection, being using to generate antibodies to detect

the presence of *S. aureus,* and being used to generate therapeutic antibodies targeting *S. aureus.*

Hybrid Polypeptides

5   Hybrid polypeptides comprise a modified ORF0657n sequence segment containing one or more alterations increasing sequence similarity to ORF0190 (SEQ ID NO: 1). The hybrid polypeptide contains one or more epitopes for ORF0657n and ORF0190.

Hybrid polypeptides can be designed taking into account the similarity
10   and differences between ORF0657n and ORF0190 proteins sequences. An amino acid alignment of ORF0657n (SEQ ID NO: 2) and ORF0190 (SEQ ID NO: 1) revealed a central region having a high degree of homology between the two proteins. The region for ORF0657n spans 327 amino acids from position 122 to 448. The ORF0190 homologous region spans 328 amino acids from position 323 to 650.
15   Within the central region, 64% of the amino acids were identical and there was an over all level of 80% similarity.

Sequence similarity was determined using a local alignment tool utilizing the program lalign (developed by Huang and Miller, *Adv. Appl. Math. 12*:337-357, 1991, for the «sim» program). The options and environment variables
20   are:-f # Penalty for the first residue a gap (-14 by default); -g # Penalty for each additional residue in a gap (-4 by default)-s str (SMATRIX) the filename of an alternative scoring matrix file. For protein sequences, PAM250 is used by default-w # (LINLEN) output line length for sequence alignments (60).

Figures 1A-1C illustrate the central region of homology between an
25   ORF0657n (SEQ ID NO: 2) and ORF0190 (SEQ ID NO: 1) and provides examples of hybrid polypeptides that can be designed taking into account ORF0657n and ORF0190 sequences. Additional hybrid polypeptides can be obtained based on the ORF0657n and ORF0190 sequence alignment provided in Figures 1A-1C, and alignments produced using other ORF0657 sequences.
30   Additional hybrids may, for example, contain one or more modifications exemplified in SEQ ID NOs: 8, 9, and 10, or additional modifications that are apparent based on different amino acid sequences for an ORF0657n variant and ORF0190. Apparent modifications are those based on aligned amino acids differing between an ORF0657n and ORF0190, where an ORF0657n amino acid is

changed to an ORF0190 amino acid. Examples of additional hybrid sequences include those provided by SEQ ID NOs: 11-43 (Figures 2A-2L).

Hybrid polypeptides may comprise modified ORF0657n sequence segments of different sizes. Preferably, the modified sequence is based on the

5   ORF0657n central region spanning amino acids 122 to 448 or a fragment thereof. In different embodiments, the modified sequence segment is at least about 100, at least about 150, at least about 200, at least about 250, or at least about 300 amino acids in length.

Reference to "modified" or "altered" ORF0657n is a structural

10   description taking into account the amino acid sequence of an ORF0657n polypeptide and ORF0190. A modified ORF0657n can be identified based on the presence of one or more stretches of at least 9 contiguous amino acids of a naturally occurring ORF0657n sequence. In different embodiments at least two, three, or four stretches of at least 9 contiguous amino acids of a naturally occurring ORF0657n sequence are

15   present in the modified sequence segment.

Examples of naturally occurring ORF0657n sequences are provided by SEQ ID NOs: 2-7. Other naturally occurring sequences can be identified based on the presence of a high degree of sequence similarity or contiguous amino acids. Contiguous amino acids provide characteristic tags. In different embodiments, a

20   naturally occurring ORF0657n sequence is a sequence found in a *Staphylococcus*, preferably *S. aureus*, having at least 20, at least 30, or at least 50 contiguous amino acids as in SEQ ID NO: 2; and/or having at least 75% sequence similarity or identity with SEQ ID NO: 2.

Sequence similarity and identity can be determined by different

25   algorithms and techniques well known in the art. Generally, sequence similarity and identity is determined by aligning two sequences to obtain maximum amino acid identity between the two sequences, allowing for gaps, additions and substitutions in one of the sequences. Sequence similarity and identity can be determined based on the differences in the aligned sequence taking into account the overall length of the

30   compared sequence.

Sequence identity can be determined by calculating the minimum number of amino acid alterations to an amino acid sequence required to arrive at a reference sequence divided by the number of amino acids in the reference sequence. Reference sequences for naturally occurring ORF0657n sequences provided herein

35   are SEQ ID NOs: 2-7 and fragments thereof.

7

Reference sequences for naturally occurring ORF0657n can also be used to determine sequence similarity. Sequence similarity can be determined, for example, as indicated above using the program lalign (developed by Huang and Miller, *Adv. Appl. Math. 12*:337-357, 1991, for the «sim» program).

5   Different numbers of alterations may be present in a modified ORF0657n sequence segment. On the one hand, as the number of alterations increases similarity to ORF0190 more ORF0190 epitopes may be present. On the other hand, increasing the number of ORF0190 epitopes may decrease the number of ORF0657n epitopes.

10   Other factors that can be taken into account for an alteration include amino acid size, charge, polarity, and hydrophobicity. The effect of different amino acid side chains on properties of an amino acid are well known in the art. (See, for example, Ausubel, *Current Protocols in Molecular Biology,* John Wiley, 1987-2001, Appendix 1C.)

15   In exchanging amino acids to maintain activity, the replacement amino acid should have one or more similar properties such as approximately the same charge and/or size and/or polarity and/or hydrophobicity. For example, substituting valine for leucine, arginine for lysine, and asparagine for glutamine are good candidates for not causing a change in polypeptide functioning.

20   In different embodiments the minimum number of alterations is 8, 20, 25, 35, 45, or 55; and the maximum number of alterations, which may be present with any of the indicated minimum number of alterations having a lower number is 50, 60, 70, 79, 90, or 100. Each alteration is independently a deletion, addition, or substitution.

25   Amino acids can be represented by different designations as follows: A=Ala=Alanine: C=Cys=Cysteine: D=Asp=Aspartic acid: E=Glu=Glutamic acid: F=Phe=Phenylalanine: G=Gly=Glycine: H=His=Histidine: I=Ile=Isoleucine: K=Lys=Lysine: L=Leu=Leucine: M=Met=Methionine: N=Asn=Asparagine: P=Pro=Proline: Q=Gln=Glutamine: R=Arg=Arginine: S=Ser=Serine:

30   T=Thr=Threonine: V=Val=Valine: W=Trp=Tryptophan: and Y=Tyr=Tyrosine.

In different embodiments the hybrid ORF0657n sequence segment comprises, consists, or consists essentially, of at least about 100 contiguous amino acids of the following Hybrid Structure:

X^1-AIKNPAI-X^2- DK-X^3-H-X^4-APN-X^5- RPIDFEMK-X^6-X^7-X^8-G-X^9-
QQFYHYAS-X^{10}-V-X^{11}- PARVIFT-X^{12}-X^{13}-K-X^{14}-IELGLQ-X^{15}-X^{16}-X^{17}-
X^{18}-W-X^{19}-KFEVYEGDKKLP-X^{20}- KLVSYD-X^{21}-X^{22}-KDYAYIRFSVSNGT-
X^{23}-X^{24}-VKIVSSTH-X^{25}-X^{26}-X^{27}-N-X^{28}-X^{29}-EKYDYTLM-X^{30}- FAQPIYN-
X^{31}-X^{32}-DK-X^{33}-X^{34}-X^{35}- EEDY-X^{36}-X^{37}-X^{38}- KLLAPYKKAKTLERQVY
EL-X^{39}- K-X^{40}- Q-X^{41}-KLPEKLKAEYKKKL-X^{42}-X^{43}-T-X^{44}- KAL-X^{45}-X^{46}-
QVKSA-X^{47}- TEFQNV-X^{48}-PTN-X^{49}-K-X^{50}- TDLQ-X^{51}-X^{52}-X^{53}-X^{54}-VV-
X^{55}-ESVEN-X^{56}-ES-X^{57}-MDTFV-X^{58}-HPIKT-X^{59}-X^{60}-LNGKKY-X^{61}-VM-
X^{62}- TTND-X^{63}-YWKDF-X^{64}- VEG-X^{65}- RVRT-X^{66}- SKD-X^{67}- KNN-X^{68}-
RT-X^{69}- IFPY-X^{70}- EGK-X^{71}-X^{72}-YDAIVKV-X^{73}- VKTI-X^{74}-Y-X^{75}-
GQYHVRI-X^{76}- DK-X^{77}-X^{78}-X^{79}

where
X^1 is either E or a D alteration;
X^2 is either K or an I alteration;
X^3 is either D or an E alteration;
X^4 is either S or a T alteration;
X^5 is either S or a W alteration;
X^6 is either K or an N alteration;
X^7 is either K or a D alteration;
X^8 is either D or a K alteration;
X^9 is either T or an E alteration;
X^{10} is either S or a T alteration;
X^{11} is either K or an E alteration;
X^{12} is either D or a K alteration;
X^{13} is either S or a T alteration;
X^{14} is either E or an I alteration;
X^{15} is either S or a T alteration;
X^{16} is either G or an A alteration;
X^{17} is either K or a S alteration;
X^{18} is either F or a T alteration;
X^{19} is either R or a K alteration;
X^{20} is either I or a V alteration;
X^{21} is either T or an S alteration;

X^{22} is either V or a D alteration;

X^{23} is either K or an R alteration;

X^{24} is either A or an E alteration;

X^{25} is either F or a Y alteration;

5 X^{26} is either an optionally present G insertion alteration;

X^{27} is either N or a E alteration;

X^{28} is either K or a I alteration

X^{29} is either E or a H alteration;

X^{30} is either E or a V alteration;

10 X^{31} is either S or a N alteration;

X^{32} is either A or a P alteration;

X^{33} is either F or an Y alteration;

X^{34} is either K or a V alteration;

X^{35} is either T or a D alteration;

15 X^{36} is either K or a N alteration;

X^{37} is either A or an L alteration;

X^{38} is either E or a Q alteration;

X^{39} is either N or an E alteration;

X^{40} is either I or a L alteration;

20 X^{41} is either D or an E alteration;

X^{42} is either E or a D alteration;

X^{43} is either D or a Q alteration;

X^{44} is either K or an R alteration;

X^{45} is either D or an A alteration;

25 X^{46} is either E or a D alteration;

X^{47} is either I or a V alteration;

X^{48} is either Q or a T alteration;

X^{49} is either E or a D alteration;

X^{50} is either M or an L alteration;

30 X^{51} is either D or an E alteration;

X^{52} is either T or an A alteration

X^{53} is either K or H alteration;

X^{54} is either Y or an F alteration;

X^{55} is either Y or an F alteration;

X^{56} is either N or a S alteration;

X^{57} is either M or a V alteration;

X^{58} is either K or an E alteration;

X^{59} is either G or an A alteration;

5   X^{60} is either M or a T alteration;

X^{61} is either M or a V alteration;

X^{62} is either E or a K alteration;

X^{63} is either D or a S alteration;

X^{64} is either M or an I alteration;

10   X^{65} is either Q or a K alteration;

X^{66} is either I or a V alteration;

X^{67} is either A or a P alteration;

X^{68} is either T or an S alteration;

X^{69} is either I or a L alteration;

15   X^{70} is either V or an I alteration;

X^{71} is either T or an A alteration;

X^{72} is either L or a V alteration;

X^{73} is either H or a V alteration;

X^{74} is either D or a G alteration;

20   X^{75} is either D or an E alteration;

X^{76} is either V or an I alteration;

X^{77} is either E or a D alteration;

X^{78} is either A or an I alteration;

X^{79} is either F or a N alteration;

25   provided that at least 20 of the alterations are present.

        With respect to the Hybrid Structure, in different embodiments the minimum number of alterations is 25, 35, 45, or 55; the maximum number of alterations, which may be present with any of the indicated minimum number of alterations having a lower number is 50, 60, 70, or 79; and/or one or more of the

30   following combinations of alterations are present:

X^{6}-X^{7}-X^{8} is either KKD or NDK alterations;

X^{17}-X^{18} is either KF or ST alterations;

X^{26}-X^{27} is either N or GE alterations;

X^{28}-X^{29} is either KE or IH alterations;

X31-X32 is either SA or NP alterations;

X34-X35 is either KT or VD alterations;

X36-X37-X38 is either KAE or NLQ alterations; and

X52-X53 is either TK or AH alterations.

5   Hybrid polypeptides may contain additional amino acid regions. Such regions should not prevent the hybrid polypeptide from providing ORF0190 and ORF0657n epitopes. Additional regions can be based on ORF0190, ORF0657n or other amino acid sequences.

Preferably, additional regions if present provide a useful purpose such 10 as providing epitopes from other bacterial polypeptides, providing an affinity tag to facilitate polypeptide purification, enhancing polypeptide efficacy, or enhancing polypeptide stability. Polypeptide production can, for example, be facilitated through the use of an initiation codon (*e.g.,* coding for methionine) suitable for recombinant expression, and the introduction of restriction enzyme recognition sites.

15   The introduction of a restriction site can be illustrated by Example 1 provided *infra* and Figure 3. For example, using the forward primer provided in Figure 3, a restriction recognition site can be introduced into a hybrid or 0657n polypeptide. The illustrated restriction site is accompanied by a glycine addition after methionine.

20   Efficacy of a polypeptide to induce an immune response can be enhanced through epitope enhancement. Epitope enhancement can be performed using different techniques such as those involving alteration of anchor residues to improve peptide affinity for MHC molecules and those increasing affinity of the peptide-MHC complex for a T-cell receptor. (Berzofsky *et al.,* 2001. *Nature Review* 25 *1*:209-219.)

Polypeptide purification can be enhanced by adding a group to the carboxy or N-terminus to facilitate purification. Examples of groups that can be used to facilitate purification include polypeptides providing affinity tags. Examples of affinity tags include a six-histidine tag, trpE, glutathione and maltose-binding protein.

30   The ability of a polypeptide to produce an immune response can be enhanced using groups that generally enhance an immune response. Examples of groups that can be joined to a polypeptide to enhance an immune response against the polypeptide include cytokines such as IL-2. (Buchan *et al.,* 2000. *Molecular Immunology 37*:545-552.)

ORF0657n Sequences

ORF0657n has been implicated to have a role in *S. aureus* iron acquisition. (Andrade *et al., Genome Biology* 3(9):47.1-47.5, 2003.) ORF0657n

5 sequences, some of which are from different sources, have been given different designations in different references. (For example, see, Etz *et al., PNAS USA,* 99:6573-6578, 2002 (LPXTGVI); Baba *et al., The Lancet 359*:1819-1827, 2002 (MW1011); Kuroda, *et al., The Lancet 357*, 1225-1240, 2001 (SA0976); Andrade *et al., Genome Biology 3(9)*:47.1-47.5, 2003 (S_aur2); Mazmanian *et al., Science*

10 *299*:906-909, 2003 (isdB); Mazmanian et al., *Molecular Microbiology 40*:1049-1057, 2001 (sasJ); and Taylor *et al., Mol. Microbiol. 43*:1603-1614, 2002 (sirH).

A polypeptide sequence corresponding to a ORF0657n protein sequence appears to be provided in different patent publications. (Meinke *et al.,* International Publication Number WO 02/059148, published August 1, 2002, Wang *et*

15 *al.,* International Publication Number WO 02/077183, published October 3, 2002, Masignani *et al.,* International Publication Number WO 02/094868, published November 28, 2002, Foster *et al.,* International Publication Number WO 02/102829, published December 27, 2002, and Foster *et al.,* International Publication Number WO 03/011899, published February 13, 2003.)

20 Additional examples of *S. aureus* ORF0657n protein sequences are provided by SEQ ID NOs: 3-7. *S. aureus* ORF0657n cDNA encoding SEQ ID NOs: 3-7 are provided by SEQ ID NOs: 52-56.

Immunogens

25 Immunogens containing a hybrid or ORF0657n polypeptide can also contain one or more additional regions or moieties joined to the polypeptide. The additional regions may be polypeptide regions or may be regions that are not polypeptides. Additional regions and moieties, if present, are preferably covalently joined to the carboxy or amino terminus of the hybrid or ORF0657n polypeptide.

30 An additional region or moiety that is present should not significantly prevent a hybrid or ORF0657n polypeptide from providing *S. aureus* epitopes that can be used for diagnostic or therapeutic purposes. Preferably, an additional region or moiety is present to achieve a particular purpose, such as to enhance polypeptide stability, purification, or the ability to produce an immune response.

Polypeptide stability can be enhanced by modifying the carboxy or N-terminus. Examples of possible modifications include amino terminus protecting groups such as acetyl, succinyl, benzyl, benzyloxycarbonyl or *t*-butyloxycarbonyl; carboxy terminus protecting groups such as amide, methylamide, and ethylamide; and
5   groups such as polyethylene glycol that may be present on the amino or carboxy terminus.

Polypeptide Production

Polypeptides can be produced using standard techniques including
10   those involving chemical synthesis and those involving purification from a cell producing the polypeptide. Techniques for chemical synthesis of polypeptides are well known in the art. (See *e.g.,* Vincent, *Peptide and Protein Drug Delivery,* New York, N.Y., Decker, 1990.)

Polypeptides can be purified from a cell using techniques well known
15   in the art. (See for example, Ausubel, *Current Protocols in Molecular Biology,* John Wiley, 1987-1998.)

Obtaining polypeptides from a cell is facilitated using recombinant nucleic acid techniques to produce the polypeptide. Recombinant nucleic acid techniques for producing a polypeptide involve introducing, or producing, a
20   recombinant gene encoding the polypeptide in a cell and expressing the polypeptide.

Recombinant nucleic acid is nucleic acid that by virtue of its sequence or form does not occur in nature. Possible forms for recombinant nucleic acid include isolation from nucleic acid found in a cell; or a combination of nucleic acid sequences not found in nature.

25   A recombinant gene contains recombinant nucleic acid encoding a polypeptide along with regulatory elements for proper transcription and processing. The encoding nucleic acid is in a form different than naturally occurring nucleic acid encoding the polypeptide. Differences in form include separation from other nucleic acid naturally associated with the encoding nucleic acid or present in a combination
30   with other nucleic acid not naturally associated with the encoding nucleic acid. The recombinant gene can be present in a cellular genome or can be part of an extrachromosomal element or vector.

The regulatory elements that may be present as part of a recombinant gene include those naturally associated with the polypeptide encoding sequence and
35   exogenous regulatory elements not naturally associated with the polypeptide

14

encoding sequence. Exogenous regulatory elements such as an exogenous promoter can be useful for expressing a recombinant gene in a particular host, or increasing the level of expression. Generally, the regulatory elements that are present in a recombinant gene include a transcriptional promoter, a ribosome binding site, a

5   terminator, and an optionally present operator. A preferred element for processing in eukaryotic cells is a polyadenylation signal.

Expression of a recombinant gene in a cell is facilitated through the use of an expression vector. Preferably, an expression vector in addition to a recombinant gene also contains an origin of replication for autonomous replication in

10   a host cell, a selectable marker, useful restriction enzyme sites, and a potential for high copy number. Examples of expression vectors are cloning vectors, modified cloning vectors, specifically designed plasmids and viruses.

Due to the degeneracy of the genetic code, a large number of different encoding nucleic acid sequences can be used to code for a particular polypeptide.

15   The degeneracy of the genetic code arises because almost all amino acids are encoded by different combinations of nucleotide triplets or "codons". Amino acids are encoded by codons as follows:

A=Ala=Alanine: codons GCA, GCC, GCG, GCU

C=Cys=Cysteine: codons UGC, UGU

20   D=Asp=Aspartic acid: codons GAC, GAU

E=Glu=Glutamic acid: codons GAA, GAG

F=Phe=Phenylalanine: codons UUC, UUU

G=Gly=Glycine: codons GGA, GGC, GGG, GGU

H=His=Histidine: codons CAC, CAU

25   I=Ile=Isoleucine: codons AUA, AUC, AUU

K=Lys=Lysine: codons AAA, AAG

L=Leu=Leucine: codons UUA, UUG, CUA, CUC, CUG, CUU

M=Met=Methionine: codon AUG

N=Asn=Asparagine: codons AAC, AAU

30   P=Pro=Proline: codons CCA, CCC, CCG, CCU

Q=Gln=Glutamine: codons CAA, CAG

R=Arg=Arginine: codons AGA, AGG, CGA, CGC, CGG, CGU

S=Ser=Serine: codons AGC, AGU, UCA, UCC, UCG, UCU

T=Thr=Threonine: codons ACA, ACC, ACG, ACU

35   V=Val=Valine: codons GUA, GUC, GUG, GUU

15

W=Trp=Tryptophan: codon UGG

Y=Tyr=Tyrosine: codons UAC, UAU

Suitable cells for recombinant nucleic acid expression of hybrid or ORF0657 polypeptides are prokaryotes and eukaryotes. Examples of prokaryotic

5   cells that can be employed include *E. coli*; members of the *Staphylococcus* genus, such as *S. aureus*; members of the *Lactobacillus* genus, such as *L. plantarum*; members of the *Lactococcus* genus, such as *L. lactis*; and members of the *Bacillus* genus, such as *B. subtilis*. Examples of eukaryotic cells that can be employed include mammalian cells; insect cells; yeast cells such as members of the *Saccharomyces*

10   genus (*e.g., S. cerevisia*) and members of the *Pichia* genus (*e.g., P. pastoris*).

Techniques for recombinant gene production, introduction into a cell, and recombinant gene expression are well known in the art. Examples of such techniques are provided in references such as Ausubel, *Current Protocols in Molecular Biology*, John Wiley, 1987-1998, and Sambrook *et al.*, *Molecular Cloning*,

15   *A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989.

If desired, expression in a particular host can be enhanced through codon optimization. Codon optimization includes using more preferred codons for the host and removal of inhibitory regions. Techniques for codon optimization in different hosts are well known in the art.

20   Preferably, a hybrid or ORF0657 polypeptide is present as a purified polypeptide. In different embodiments, the purified polypeptide represents at least about 10%, at least about 50%, at least about 75%, or at least about 95% of the total protein in a sample or preparation. Reference to "purified polypeptide" does not require that the polypeptide has undergone any purification and may include, for

25   example, chemically synthesized polypeptide that has not been purified.

Adjuvants

Adjuvants are substances that can assist an immunogen in producing an immune response. Adjuvants can function by different mechanisms such as one or

30   more of the following: increasing the antigen biologic or immunologic half-life; improving antigen delivery to antigen-presenting cells; improving antigen processing and presentation by antigen-presenting cells; and inducing production of immunomodulatory cytokines. (Vogel, *Clinical Infectious Diseases 30*(suppl. 3):S266-270, 2000.)

A variety of different types of adjuvants can be employed to assist in the production of an immune response. Examples of particular adjuvants include aluminum hydroxide, aluminum phosphate, other salts of aluminum, calcium phosphate, DNA CpG motifs, monophosphoryl lipid A, cholera toxin, *E. coli* heat-

5 labile toxin, pertussis toxin, muramyl dipeptide, Freund's incomplete adjuvant, MF59, SAF, immunostimulatory complexes, liposomes, biodegradable microspheres, saponins, nonionic block copolymers, muramyl peptide analogues, polyphsophazene, synthetic polynucleotides, IFN-γ, IL-2 and IL-12. (Vogel *Clinical Infectious Diseases 30*(suppl 3):S266-270, 2000, Klein *et al., Journal of Pharmaceutical Sciences 89,*

10 311-321, 2000.)

Patients For Inducing Protective Immunity

A "patient" refers to a mammal capable of being infected with *S. aureus*. A patient can be treated prophylactically or therapeutically. Prophylactic

15 treatment provides sufficient protective immunity to reduce the likelihood, or severity, of a *S. aureus* infection. Therapeutic treatment can be performed to reduce the severity of a *S. aureus* infection.

Prophylactic treatment can be performed using a vaccine containing an immunogen described herein. Such treatment is preferably performed on a human.

20 Vaccines can be administered to the general population or to those persons at an increased risk of *S. aureus* infection.

Persons with an increased risk of *S. aureus* infection include health care workers; hospital patients; patients with a weakened immune system; patients undergoing surgery; patients receiving foreign body implants, such a catheter or a

25 vascular device; patients facing therapy leading to a weakened immunity; and persons in professions having an increased risk of burn or wound injury. (*The Staphylococci in Human Disease*, Crossley and Archer (ed.), Churchill Livingstone Inc. 1997.)

Non-human patients that can be infected with *S. aureus* include horses, cows, pigs, sheep, goats, rabbits, horses, dogs, cats and mice. Treatment of non-

30 human patients is useful in protecting pets and livestock, and in evaluating the efficacy of a particular treatment.

Combination Vaccines

Hybrid or ORF0657 polypeptides can be used alone, or in combination

35 with other immunogens, to induce an immune response. Additional immunogens that

17

may be present include: one or more additional *S. aureus* immunogens, such as those referenced in the Background of the Invention *supra*; one or more immunogens targeting one or more other *Staphylococcus* organisms such as *S. epidermidis, S. haemolyticus, S. warneri,* or *S.lugunensis*; and one or more immunogens targeting

5   other infections organisms.

Animal Model System

An animal model system was developed to evaluate the efficacy of an immunogen to produce a protective immune response against *Staphylococcus*. Two

10   obstacles encountered in setting up a protective animal model were: (1) very high challenge dose needed to overcome innate immunity and (2) death rate too fast to detect a protective response. Specifically, after bacterial challenge mice succumbed to infection within 24 hours which did not provide sufficient time for the specific immune responses to resolve the infection. If the dose was lowered both control and

15   immunized mice survived the infection.

These obstacles were addressed by developing a slow kinetics lethality model involving *Staphylococcus* prepared from cells in stationary phase, appropriately titrated, and intravenously administered. This slow kinetics of death provides sufficient time for the specific immune defense to fight off the bacterial

20   infection (*e.g.,* 10 days rather 24 hours).

Staphylococcus cells in stationary phase can be obtained from cells grown on solid medium. They can also be obtained from liquid, however the results with cells grown on solid media were more reproducible. Cells can conveniently be grown overnight on solid medium. For example, *S. aureus* can be grown from about

25   18 to about 24 hours under conditions where the doubling time is about 20-30 minutes.

Staphylococcus can be isolated from solid or liquid medium using standard techniques to maintain *Staphylococcus* potency. Isolated *Staphylococcus* can be stored, for example, at -70°C as a washed high density suspension (> 10^9

30   colony forming units (CFU)/mL) in phosphate buffered saline containing glycerol.

The *Staphylococcus* challenge should have a potency providing about 80 to 90% death in an animal model over a period of about 7 to10 days starting on the first or second day. Titration experiments can be performed using animal models to monitor the potency of the stored *Staphylococcus* inoculum. The titration

18

experiments can be performed about one to two weeks prior to an inoculation experiment.

Initial potency for titration experiments can be based on previous experiments. For *S. aureus* and the animal model strain Becker a suitable potency 5 was generally found in the range of 5 x 10^8 to 8 x 10^8 CFU/ml.

Different types of *Staphylococcus* can be evaluated in the animal model, such as *S. aureus, S. epidermidis, S. haemolyticus, S. warneri,* or *S.lugunensis.* In a preferred embodiment the *Staphylococcus* is *S. aureus.*

10 Administration

Immunogens can be formulated and administered to a patient using the guidance provided herein along with techniques well known in the art. Guidelines for pharmaceutical administration in general are provided in, for example, *Vaccines* Eds. Plotkin and Orenstein, W.B. Sanders Company, 1999; *Remington's Pharmaceutical* 15 *Sciences 20th Edition,* Ed. Gennaro, Mack Publishing, 2000; and *Modern Pharmaceutics 2nd Edition,* Eds. Banker and Rhodes, Marcel Dekker, Inc., 1990, each of which are hereby incorporated by reference herein.

Pharmaceutically acceptable carriers facilitate storage and administration of an immunogen to a patient. Pharmaceutically acceptable carriers 20 may contain different components such as a buffer, sterile water for injection, normal saline or phosphate buffered saline, sucrose, histidine, salts and polysorbate.

Immunogens can be administered by different routes such as subcutaneous, intramuscular, or mucosal. Subcutaneous and intramuscular administration can be performed using, for example, needles or jet-injectors.

25 Suitable dosing regimens are preferably determined taking into account factors well known in the art including age, weight, sex and medical condition of the patient; the route of administration; the desired effect; and the particular compound employed. The immunogen can be used in multi-dose vaccine formats. It is expected that a dose would consist of the range of 1 μg to 1.0 mg total 30 polypeptide, in an embodiment of the present invention the range is 0.1 mg to 1.0 mg.

The timing of doses depends upon factors well known in the art. After the initial administration one or more booster doses may subsequently be administered to maintain or boost antibody titers. An example of a dosing regime would be day 1, 1 month, a third dose at either 4, 6 or 12 months, and additional 35 booster doses at distant times as needed.

Generation of Antibodies

A hybrid or ORF0657 polypeptide can be used to generate antibodies and antibody fragments that bind to the polypeptide or to *S. aureus*. Such antibodies and antibody fragments have different uses including use in polypeptide purification,

5   *S. aureus* identification, or in therapeutic or prophylactic treatment against *S. aureus* infection.

Antibodies can be polyclonal or monoclonal. Techniques for producing and using antibodies are well known in the art. Examples of such techniques are described in Ausubel, *Current Protocols in Molecular Biology*, John

10   Wiley, 1987-1998, Harlow *et al., Antibodies, A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, and Kohler *et al., Nature 256*:495-497, 1975.

EXAMPLES

Examples are provided below further illustrating different features of

15   the present invention. The examples also illustrate useful methodology for practicing the invention. These examples do not limit the claimed invention.

Example 1: Use of ORF0657n to Provide Protective Immunity

This example illustrates the ability of ORF0657n to provide protective

20   immunity in a model.

Mutated ORF 0657n Cloning and Expression

An ORF0657n DNA sequence (SEQ ID NO: 23) was translated using Vector NTI software and the resulting 645 amino acid sequence (SEQ ID NO: 2) was

25   analyzed. PCR primers were designed to amplify the gene starting at the first asparagine residue and ending prior to the stop codon at the terminal asparagine residue (Figure 3). These PCR primers also had additional NcoI (forward primer) and XhoI (reverse primer) sites to facilitate cloning into the expression vector.

The protein was designed to be expressed from the pET28 vector with

30   the terminal His residues and the stop codon encoded by the vector. In addition, a glycine residue was added to the protein after the methionine initiator. The resulting amplified (1964 bp) DNA sequence encodes a 654 amino acid mutated form of mature ORF 0657n (Figure 4a). Figure 4B shows an alignment of the translation of the native 0657n ORF with that of the expressed construction.

PCR amplified sequences were ligated into the pET28 vector (Novagen) using the NcoI/XhoI sites that had been engineered into the PCR primers and introduced into *E. coli* DH5α (Invitrogen) by heat shock. Colonies were selected, grown in LB with 30 µg/mL kanamycin, DNA minipreps made (Promega), and insert

5   integrity determined by restriction digestion and PCR. Four minipreps with correct insert size were sequenced using the primers listed in Table 1. A clone was selected containing no DNA changes from the desired sequence.

Table 1

10

SEQ ID NO:	Description	Sequence
50	M13F	5'-CTGGCCGTCGTTTTAC
51	M13R	5'-CAGGAAACAGCTATGAC
46	ORF0657nF	5'-AACCGGTTTTCCATGGGGAACAAA CAGCAAAAAGAATTT-3'
48	ORF0657nR	5'- ACCGGTTTCTCGAGTTAGTTTTTA CGTTTTCTAGGTAATAC-3'

E. coli HMS174(DE3) cells (Novagen) were transformed and grown on LB plates containing kanamycin (30ug/ml); 3 colonies (UnkC-1, UnkC-2 and UnkC-3) were selected for expression testing. Liquid LB (kanamycin) cultures were

15   incubated at 37°C, 250 rpm until the A_{600} was between 0.6 and 1.0 and then induced by the addition of IPTG to final concentrations of 1 mM followed by three hours further incubation. Cultures were harvested by centrifugation at 5000 x g for 5 minutes at 4°C. Cells were resuspended in 500 µl lysis buffer (Bug Buster, with protease inhibitors, Novagen). An equal volume of loading buffer (supplemented with

20   β-mecapto ethanol to 5% final volume) was added prior to heating the samples at 70°C for 5 minutes. Extracts were run on Novex 4-20% Tris-Glycine gels and assayed for protein (Coomassie Blue stained) and blotted onto nitrocellulose and probed with anti-HIS6 antibodies (Zymedd).

25   *Mutated ORF0657n Purification*

Direct scale-up of the above small scale procedure into stirred tank fermenters (75 liter scale) with a 50 liter working volume was achieved. Inoculum

was cultivated in a 250 mL flask containing 50 mL of Luria-Bertani (LB) medium (plus Kanamycin) and inoculated with 1 mL of frozen seed culture and cultivated for 3 hours. One mL of this seed was used to inoculate a 2 liter flask containing 500 mL of LB medium (plus Kanamycin) and incubated for 16 hours. A large scale fermenter

5 (75 liter scale) was cultivated with 50 liters of LB medium (plus Kanamycin). The fermentation parameters of the fermenter were: pressure = 5 psig, agitation speed = 300 RPMs, airflow = 15 liters/minute and temperature = 37oC. Cells were incubated to an optical density (OD) of 0.8 optical density units, at a wavelength of 600nm, and induced with Isopropyl-B-K-Thiogalactoside (IPTG) at a concentration of 1 mM.

10 Induction time, with IPTG, was three hours. Cells were harvested by lowering the temperature to 15oC, concentration through a 500KMWCO hollow fiber cartridge, and centrifuged at 9,000 times gravity at 4oC for 20 minutes. Supernates were decanted and the recombinant E. coli wet cell pellets were frozen at –70oC.

Recombinant $E.\ coli$ cells (19.2 grams wet cell weight) were

15 suspended in Lysis Buffer (50 mM Tris-HCl, pH 8.0, 0.1 M NaCl, 2 mM MgCl$_2$, 10 mM imidazole, 0.1% Tween™-80, and 6 M guanidine-HCl) at 8 ml per gram of cell wet weight. Protease Inhibitor Cocktail for use with poly-(Histidine)-tagged proteins (Sigma, P8849) was added to the suspension at 0.05 ml per gram of cell paste. Additionally, Lysozyme was added to 1 mg/mL, and Benzonase™ (EM Ind.) was

20 added to 1 µL/mL. Cell lysis was accomplished by passing the suspension through a microfluidizer at 14,000 PSI (Microfluidics Model 110S) four times at 4°C. Cell debris was pelleted at 11,000 x g for 30 minutes at 4°C, and the supernatant retained.

Proteins bearing a His-tag were purified from the supernatant. The supernatant was mixed with 20 mL of Ni$^+$-NTA agarose (Qiagen) at 4°C with gentle

25 inversion for 2 hours. The mixture was poured into an open column (1.5 cm x 20 cm) and the non-bound fraction was collected in bulk. The column was washed with Wash Buffer (20 mM Tris-HCl, pH 8.0, 0.15 M NaCl, 0.1% Tween™-80). His-tagged ORF0657n was eluted with a step gradient of 300 mM imidazole, 20 mM Tris-HCl, pH 7.5, 0.15 M NaCl, 0.1% Tween™-80.

30 Fractions containing mutated ORF0657n were detected by Coomassie stained SDS-PAGE and pooled. Pooled fractions were filtered through a 0.2 micron filter to remove particulate material, and were applied on a size-exclusion column (Sephacryl S-300 26/60 column, Amersham Biosciences) and eluted at 1 mL/min with 10 mM MOPS pH 7.1, 150 mM NaCl. Fractions containing mutated ORF0657n

35 were detected by Coomassie stained SDS-PAGE and Western blotting (anti-tetra His

Mab, Qiagen). Endotoxin was removed by filtration through a Zeta-Plus™ Biofilter (CUNO). Protein was determined by BCA (Pierce). Purity was determined by densitometry of Coomassie stained gels.

5   *Preparation of S. Aureus Challenge*

S. aureus was grown on TSA plates at 37°C overnight. The bacteria were washed from the TSA plates by adding 5 ml of PBS onto a plate and gently resuspending the bacteria with a sterile spreader. The bacterial suspension was spun at 6000 rpm for 20 minutes using a Sorvall RC-5B centrifuge (DuPont Instruments).

10   The pellet was resuspended in 16% glycerol and aliquots were stored frozen at –70°C.

Prior to use, inocula were thawed, appropriately diluted and used for infection. Each stock was titrated at least 3 times to determine the appropriate dose inducing slow kinetics of death in naive mice. The potency of the bacterial inoculum (80 to 90% lethality) was constantly monitored to assure reproducibility of the model.

15   Ten days before each challenge experiment, a group of 10 control animals (immunized with adjuvant alone) were challenged and monitored.

Protection Studies for Mutated ORF0657n

Twenty-five BALB/c mice were immunized with three doses of

20   mutated ORF0657n (20 µg per dose) on aluminum hydroxyphosphate adjuvant (450 µg per dose). Aluminum hydroxyphosphate adjuvant (AHP) is described by Klein *et al., Journal of Pharmaceutical Sciences 89*, 311-321, 2000. The doses were administered as two 50 µl injections on days 0, 7 and 21. The mice were bled on day 28, and their sera were screened by ELSIA for reactivity to mutated ORF0657n.

25   On day 35 of the experiment the mice were challenged by intravenous injection of *S. aureus* grown at a dose (7.3 x 10^8 CFU ml) determined in titration experiments to cause death over a period of approximately 2 to 7 days. Survival in this lethal model with slow kinetics of death was evaluated against a control set of mice that had just been sham-immunized with AHP. The mice were monitored over a

30   14 day period for survival (Figure 5). At the end of the experiment 11 mice survived the ORF 0657n immunized group compared to three surviving in the AHP control group.

Example 2: Obtaining ORF0657n Sequences.

Different *S. aureus* clinical isolates were added to 3 ml of Difco Tryptic Soy Broth (Becton Dickinson, Sparks, MD) and incubated overnight at 37^0C and 150 rpm. The overnight cultures were centrifuged in 1.5 ml Eppendorf tubes at

5   14,000 rpm for 5 minutes. The broth was decanted and the pellets re-suspended in 500 μl re-suspension buffer (25% sucrose, 10 mM Tris pH 7.5). A 5 μl of a 2 mg/ml lysostaphin (Sigma-Aldrich, St. Louis, MO) solution was added to each resuspended pellet. Suspensions were then incubated at 37^0C for 1 hour. At the end of the incubation period, 250 μl of 2% SDS was added to each tube and vortexed until the

10   viscosity of the solution noticeably decreased. 250 μl phenol-chloroform-isoamyl solution (25:24:1, v/v) (Gibco/Invitrogen Corporation, Grand Island, NY) were added. The mixture was vortexed for 30 seconds and centrifuged for 5 minutes at 14,000 rpm. The top aqueous phase was removed and the precipitation steps were repeated until barely any interface remained. 0.1 volume of 3 M NaOAc, pH 4.8, was

15   added to each tube and mixed. One volume of isopropanol was then added and mixed again. The tubes were left to incubate 5 minutes at room temperature and then centrifuged at 14,000 rpm for 15 minutes. The supernatant was decanted and tubes were allowed to dry upside-down on tissue. The pellets were resuspended in 50 μl sterile H_2O.

20   The isolated DNA was used as a template for PCR. The gene was amplified using the following PCR primers: forward primer (SEQ ID NO: 46) and reverse primer (SEQ ID NO: 48). PCR products were sequenced using standard Big Dye protocols.

25   Other embodiments are within the following claims. While several embodiments have been shown and described, various modifications may be made without departing from the spirit and scope of the present invention.

WHAT IS CLAIMED IS:

1.   A hybrid polypeptide comprising a modified ORF0657n
sequence segment at least about 100 amino acids in length, wherein said modified
5   sequence segment comprises one or more alterations that increases sequence
similarity to SEQ ID NO: 1.

2.   The hybrid polypeptide of claim 1, wherein said modified
sequence segment comprises at least about 100 amino acids of a modified amino acid
10   sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ
ID NO: 4, SEQ ID NO: 5, and SEQ ID NO: 6, provided that said modified amino acid
sequence contains at least 8 amino acid alterations that increase sequence similarity to
SEQ ID NO: 1.

15   3.   The hybrid polypeptide of claim 3, wherein said modified
amino acid sequence is SEQ ID NO: 2 containing 8 to 100 amino acid alterations that
increase sequence similarity to SEQ ID NO: 1.

4.   The hybrid polypeptide of claim 2, wherein said modified
20   amino acid sequence has the following sequence:
X^1-AIKNPAI-X^2- DK-X^3-H-X^4-APN-X^5- RPIDFEMK-X^6-X^7-X^8-G-X^9-
QQFYHYAS-X^{10}-V-X^{11}- PARVIFT-X^{12}-X^{13}-K-X^{14}-IELGLQ-X^{15}-X^{16}-X^{17}-
X^{18}-W-X^{19}-KFEVYEGDKKLP-X^{20}- KLVSYD-X^{21}-X^{22}-KDYAYIRFSVSNGT-
X^{23}-X^{24}-VKIVSSTH-X^{25}-X^{26}-X^{27}-N-X^{28}-X^{29}-EKYDYTLM-X^{30}- FAQPIYN-
25   X^{31}-X^{32}-DK-X^{33}-X^{34}-X^{35}- EEDY-X^{36}-X^{37}-X^{38}- KLLAPYKKAKTLERQVY
EL-X^{39}- K-X^{40}- Q-X^{41}-KLPEKLKAEYKKKL-X^{42}-X^{43}-T-X^{44}- KAL-X^{45}-X^{46}-
QVKSA-X^{47}- TEFQNV-X^{48}-PTN-X^{49}-K-X^{50}- TDLQ-X^{51}-X^{52}-X^{53}-X^{54}-VV-
X^{55}-ESVEN-X^{56}-ES-X^{57}-MDTFV-X^{58}-HPIKT-X^{59}-X^{60}-LNGKKY-X^{61}-VM-
X^{62}- TTND-X^{63}-YWKDF-X^{64}- VEG-X^{65}- RVRT-X^{66}- SKD-X^{67}- KNN-X^{68}-
30   RT-X^{69}- IFPY-X^{70}- EGK-X^{71}-X^{72}-YDAIVKV-X^{73}- VKTI-X^{74}-Y-X^{75}-
GQYHVRI-X^{76}- DK-X^{77}-X^{78}-X^{79}

wherein
X^1 is either E or a D alteration;
35   X^2 is either K or an I alteration;

25

X^3 is either D or an E alteration;

X^4 is either S or a T alteration;

X^5 is either S or a W alteration;

X^6-X^7-X^8 is either KKD or NDK alterations;

5   X^9 is either T or an E alteration;

X^{10} is either S or a T alteration;

X^{11} is either K or an E alteration;

X^{12} is either D or a K alteration;

X^{13} is either S or a T alteration;

10   X^{14} is either E or an I alteration;

X^{15} is either S or a T alteration;

X^{16} is either G or an A alteration;

X^{17}-X^{18} is either KF or ST alterations;

X^{19} is either R or a K alteration;

15   X^{20} is either I or a V alteration;

X^{21} is either T or an S alteration;

X^{22} is either V or a D alteration;

X^{23} is either K or an R alteration;

X^{24} is either A or an E alteration;

20   X^{25} is either F or a Y alteration;

X^{26}-X^{27} is either N or GE alterations;

X^{28}-X^{29} is either KE or IH alterations;

X^{30} is either E or a V alteration;

X^{31}-X^{32} is either SA or NP alterations;

25   X^{33} is either F or an Y alteration;

X^{34}-X^{35} is either KT or VD alterations;

X^{36}-X^{37}-X^{38} is either KAE or NLQ alterations;

X^{39} is either N or an E alteration;

X^{40} is either I or a L alteration;

30   X^{41} is either D or an E alteration;

X^{42} is either E or a D alteration;

X^{43} is either D or a Q alteration;

X^{44} is either K or an R alteration;

X^{45} is either D or an A alteration;

X^{46} is either E or a D alteration;

X^{47} is either I or a V alteration;

X^{48} is either Q or a T alteration;

X^{49} is either E or a D alteration;

5   X^{50} is either M or an L alteration;

X^{51} is either D or an E alteration;

X^{52}-X^{53} is either TK or AH alterations;

X^{54} is either Y or an F alteration;

X^{55} is either Y or an F alteration;

10   X^{56} is either N or a S alteration;

X^{57} is either M or a V alteration;

X^{58} is either K or an E alteration;

X^{59} is either G or an A alteration;

X^{60} is either M or a T alteration;

15   X^{61} is either M or a V alteration;

X^{62} is either E or a K alteration;

X^{63} is either D or a S alteration;

X^{64} is either M or an I alteration;

X^{65} is either Q or a K alteration;

20   X^{66} is either I or a V alteration;

X^{67} is either A or a P alteration;

X^{68} is either T or an S alteration;

X^{69} is either I or a L alteration;

X^{70} is either V or an I alteration;

25   X^{71} is either T or an A alteration;

X^{72} is either L or a V alteration;

X^{73} is either H or a V alteration;

X^{74} is either D or a G alteration;

X^{75} is either D or an E alteration;

30   X^{76} is either V or an I alteration;

X^{77} is either E or a D alteration;

X^{78} is either A or an I alteration;

X^{79} is either F or a N alteration;

provided that at least 20 of said alterations are present.

27

5.   The hybrid polypeptide of claim 4, wherein said modified sequence segment comprises at least 200 amino acids of said modified amino acid sequence.

5

6.   The hybrid polypeptide of claim 5, wherein said modified sequence segment comprises said modified amino acid sequence and at least 55 of said alterations are present.

10   7.   The hybrid polypeptide of claim 1, wherein said hybrid polypeptide consists of a sequence selected from the group consisting of SEQ ID NOs: 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, and 43.

15   8.   A method of making a hybrid polypeptide comprising the step of introducing one or more alterations into a ORF0657n sequence segment at least about 100 amino acids in length, wherein at least one of said alterations increases sequence similarity to SEQ ID NO: 1.

20   9.   An isolated polypeptide comprising an amino acid sequence selected the group consisting of: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, and SEQ ID NO: 7.

10.   A polypeptide comprising amino acids 2-646 of SEQ ID NO:
25   45.

11.   The polypeptide of claim 10, wherein said polypeptide consists of either amino acids 1-646 of SED ID NO: 44 or 2-646 of SEQ ID NO: 44.

30   12.   An immunogen comprising a polypeptide that induces protective immunity against *Staphylococcus aureus*, wherein said polypeptide is either:

      a) the hybrid polypeptide of any one of claims 1-7; or
      b) the polypeptide of any one of claims 9-11.

35

28

13.   The immunogen of claim 12, wherein said immunogen consists of said polypeptide and an optionally present region or moiety, wherein said region or moiety, if present, is covalently joined to said polypeptide at the carboxy or amino terminus and said region or moiety has at least one of the following properties:
5   enhances the immune response, facilitates purification, or facilitates polypeptide stability.

14.   The immunogen of claim 13, wherein said immunogen consists of said polypeptide joined to said region or moiety.
10

15.   A composition able to induce a protective immune response in a patient comprising an immunologically effective amount of the immunogen of claim 12 and a pharmaceutically acceptable carrier.

15   16.   The composition of claim 15, wherein said composition further comprises an adjuvant.

17.   A method of inducing a protective immune response in a patient comprising the step of administering to said patient an immunologically
20   effective amount of the immunogen claim 12.

18.   The method of claim 17, wherein said patient is either a cow, pig, sheep, goat, rabbit, horse, dog, or cat.

25   19.   The method of claim 17, wherein said patient is a human.

20.   The method of claim 17, wherein said patient is being treated prophylactically against *S. aureus* infection.

30   21.   A method of inducing a protective immune response in a patient comprising the step of administering to said patient an immunologically effective amount of the composition of claim 16.

22.   The method of claim 21, wherein said patient is either a cow,
35   pig, sheep, goat, rabbit, horse, dog, or cat.

29

23. The method of claim 21, wherein said patient is a human.

24. A nucleic acid comprising a nucleotide sequence encoding the polypeptide of any one of claims 1-7, 10 and 11.

25. The nucleic acid of claim 24, wherein said nucleic acid is an expression vector and said nucleotide sequence is part of a recombinant gene.

26. A cell comprising the recombinant gene of claim 25, wherein said recombinant gene expresses said nucleic acid sequence in said cell to produce said polypeptide.

27. A recombinant nucleic acid comprising a nucleotide sequence encoding the polypeptide of claim 9.

28. The recombinant nucleic acid of claim 27, wherein said nucleic acid is an expression vector and said nucleotide sequence is part of a recombinant gene.

29. A cell comprising the recombinant gene of claim 28, wherein said recombinant gene expresses said nucleic acid sequence in said cell to produce said polypeptide.

30. A method for evaluating the efficacy of an immunogen to produce a protective immune response against *Staphylococcus* comprising the steps of:

(a) inoculating an animal model with said immunogen to produce an immunized animal model;

(b) challenging said immunized animal model with a *Staphylococcus* challenge at a potency that provides about 80 to 90% death in said animal model over a period of about 7 to 10 days starting on the first or second day, wherein said *Staphylococcus* challenge is produced from *Staphylococcus* grown to stationary phase, and said *Staphylococcus* challenge is intravenously introduced into said immunized animal model; and

30

(c) measuring the ability of said immunogen to provide protective immunity.

31. The method of claim 30, wherein said animal model is a rat or mouse.

32. The method of claim 31, wherein said *Staphylococcus* grown to stationary phase is produced on solid media.

33. The method of claim 32, wherein said *Staphylococcus* is grown about 18 to 24 hours with a doubling about 20-30 minutes.

34. The method of claim 33, wherein said *Staphylococcus* is *Staphylococcus aureus*.

35. The method of claim 34, wherein said immunogen is the immunogen of claim 12.

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TITLE OF THE INVENTION
POLYPEPTIDES FOR INDUCING A PROTECTIVE IMMUNE RESPONSE
AGAINST *STAPHYLOCOCCUS AUREUS*

5   ABSTRACT OF THE DISCLOSURE

The present invention features hybrid polypeptides providing
ORF0657n and ORFO190 epitopes, ORF0657n polypeptides, nucleic acid encoding
for the different polypeptides, and a method for evaluating the ability of an
immunogen to produce a protective immune response against *Staphylococcus*
10   infection. ORF0657n and ORF0190 are both *S. aureus* proteins.

```
0657n          MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNT-----EAQ--
0657nHybrid1   MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNT-----EAQ--
0657nHybrid2   MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNT-----EAQ--
0657nhybrid3   MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNT-----EAQ--
ORF0190        MNKHHPKLRSFYSIRKSTLGVASVIVSTLFLITSQHQAQAA--EN--TNTSDKISENQNN


0657n          -------PKTEAVASPTTT------------SEK------APETK-------------
0657nHybrid1   -------PKTEAVASPTTT------------SEK------APETK-------------
0657nHybrid2   -------PKTEAVASPTTT------------SEK------APETK-------------
0657nhybrid3   -------PKTEAVASPTTT------------SEK------APETK-------------
ORF0190        NATTTQPPKDTNQTQPATQPANTAKNYPAADESLKDAIKDPALENKEHDIGPREQVNFQL


0657n          -----------------------------------------------------PVANAVSV
0657nHybrid1   -----------------------------------------------------PVANAVSV
0657nHybrid2   -----------------------------------------------------PVANAVSV
0657nhybrid3   -----------------------------------------------------PVANAVSV
ORF0190        LDKNNETQYYHFFSIKDPADVYYTKKKAEVELDINTASTWKKFEVYENNQKLPVR-LVSY


0657n          SNK-EVEA----PTS-ETKEAKEV--------------KEVKAP---KETKEVK----
0657nHybrid1   SNK-EVEA----PTS-ETKEAKEV--------------KEVKAP---KETKEVK----
0657nHybrid2   SNK-EVEA----PTS-ETKEAKEV--------------KEVKAP---KETKEVK----
0657nhybrid3   SNK-EVEA----PTS-ETKEAKEV--------------KEVKAP---KETKEVK----
ORF0190        SPVPEDHAYIRFPVSDGTQELKIVSSTQIDDGEETNYDYTKLVFAKPIYNDPSLVKSDTN


0657n          ----------------------------------------------PA-------------
0657nHybrid1   ----------------------------------------------PA-------------
0657nHybrid2   ----------------------------------------------PA-------------
0657nhybrid3   ----------------------------------------------PA-------------
ORF0190        DAVVTNDQSSSVASNQTNTNTSNQNTSTINNANNQPQATTNMSQPAQPKSSTNADQASSQ


0657n          -AKATN---NT---------------YPILNQELREAIKNPAIKDKDHSAPNSRPIDFE
0657nHybrid1   -AKATN---NT---------------YPILNQELREAIKNPAIIDKDHSAPNWRPIDFE
0657nHybrid2   -AKATN---NT---------------YPILNQELREAIKNPAIKDKEHSAPNSRPIDFE
0657nhybrid3   -AKATN---NT---------------YPILNQELRDAIKNPAIKDKEHTAPNSRPIDFE
ORF0190        PAHETNSNGNTNDKTNESSNQSDVNQQYPPADESLQDAIKNPAIIDKEHTADNWRPIDFQ
```

Fig. 1A

```
0657n          MKKKDGTQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSY
0657nHybridl   MKNDKGEQQFYHYASSVEPARVIFTKSKPIIELGLQSASTWKKFEVYEGDKKLPIKLVSY
0657nHybrid2   MKKKDGTQQFYHYASSVKPARVIFTDSKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSY
0657nhybrid3   MKKKDGTQQFYHYASTVKPARVIFTDTKPEIELGLQTAQFWKKFEVYEGDKKLPVKLVSY
ORF0190        MKNDKGERQFYHYASTVEPATVIFTKTGPIIELGLKTASTWKKFEVYEGDKKLPVELVSY


0657n          DTVKDYAYIRFSVSNGTKAVKIVSSTHF-NNKEEKYDYTLMEFAQPIYNSADKFKTEEDY
0657nHybridl   DSDKDYAYIRFSVSNGTKEVKIVSSTHFGENIHEKYDYTLMVFAQPIYNNPDKFVDEEDY
0657nHybrid2   DTVKDYAYIRFSVSNGTKAVKIVSSTHF-NNKEEKYDYTLMEFAQPIYNSADKFKTEEDY
0657nhybrid3   DSVKDYAYIRFSVSNGTRAVKIVSSTHY-NNKEEKYDYTLMEFAQPIYNSADKYKTEEDY
ORF0190        DSDKDYAYIRFPVSNGTREVKIVSSIEYGENIHEDYDYTLMVFAQPITNNPDDYVDEETY


0657n          KAEKLLAPYKKAKTLERQVYELNKIQDKLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQ
0657nHybridl   NLQKLLAPYKKAKTLERQVYELEKIQDKLPEKLKAEYKKKLDQTKKALADQVKSAITEFQ
0657nHybrid2   KAEKLLAPYKKAKTLERQVYELNKLQEKLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQ
0657nhybrid3   KAEKLLAPYKKAKTLERQVYELNKLQEKLPEKLKAEYKKKLDDTRKALDDQVKSAVTEFQ
ORF0190        NLQKLLAPYHKAKTLERQVYELEKLQEKLPEKYKAEYKKKLDQTRVELADQVKSAVTEFE


0657n          NVQPTNEKMTDLQDTKYVVYESVENNESMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWK
0657nHybridl   NVTPTNDKLTDLQDAHFVVFESVENSESMMDTFVEHPIKTATLNGKKYMVMKTTNDSYWK
0657nHybrid2   NVQPTNDKMTDLQDTKYVVYESVENNESMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWK
0657nhybrid3   NVQPTNDKLTDLQETKFVVFESVENNESVMDTFVKHPIKTAMLNGKKYVVMETTNDDYWK
ORF0190        NVTPTNDQLTDLQEAHFVVFESEENSESVMDGFVEHPFYTATLNGQKYVVMKTKDDSYWK


0657n          DFMVEGQRVRTISKDAKNNTRTIIFPYVEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEA
0657nHybridl   DFIVEGKRVRTISKDPKNNSRTIIFPYIEGKALYDAIVKVVVKTIGYDGQYHVRIIDKDI
0657nHybrid2   DFMVEGQRVRTISKDAKNNTRTLIFPYIEGKTLYDAIVKVHVKTIDYEGQYHVRIVDKEA
0657nhybrid3   DFIVEGQRVRTVSKDAKNNSRTLIFPYIEGKTVYDAIVKVHVKTIDYEGQYHVRIIDKDA
ORF0190        DLIVEGKRVTTVSKDPKNNSRTLIFPYIPDKAVYNAIVKVVVANIGYEGQYHVRIINQDI


0657n          FTKANTDKS--NKKE---QQDNSAKKEATP--------ATPSKPTPSP----VEKESQKQ
0657nHybridl   NTKANTDKS--NKKE---QQDNSAKKEATP-------ATPSKPTPSP----VEKESQKQ
0657nHybrid2   FTKANTDKS--NKKE---QQDNSAKKEATP-------ATPSKPTPSP----VEKESQKQ
0657nhybrid3   FTKANTDKS--NKKE---QQDNSAKKEATP-------ATPSKPTPSP----VEKESQKQ
ORF0190        NTKD-DDTSQNNTSEPLNVQTGQEGKVADTDVAENSSTATNPK-DASDKADVIEPES---
```

Fig. 1B

```
0657n          DSQKD-DN---K--QLPSVEKENDASSESGKDK-------TPATKPTKG--------EVE
0657nHybrid1   DSQKD-DN---K--QLPSVEKENDASSESGKDK-------TPATKPTKG--------EVE
0657nHybrid2   DSQKD-DN---K--QLPSVEKENDASSESGKDK-------TPATKPTKG--------EVE
0657nhybrid3   DSQKD-DN---K--QLPSVEKENDASSESGKDK-------TPATKPTKG--------EVE
ORF0190        DVVKDADNNIDKDVQHD-VDHLSDMSDNNHFDKYDLKEMDTQIAKDTDRNVDKDADNSVG


0657n          SSSTTPTKVVSTTQNVAKPTTASSKTTKD-VVQT--------SAGSSEAKDSAPLQKAN-
0657nHybrid1   SSSTTPTKVVSTTQNVAKPTTASSKTTKD-VVQT--------SAGSSEAKDSAPLQKAN-
0657nHybrid2   SSSTTPTKVVSTTQNVAKPTTASSKTTKD-VVQT-------SAGSSEAKDSAPLQKAN-
0657nhybrid3   SSSTTPTKVVSTTQNVAKPTTASSKTTKD-VVQT-------SAGSSEAKDSAPLQKAN-
ORF0190        MSS-----------NVD--TDKDSNKNKDKVIQLNHIADKNNHTG-KAAKLDVVKQNYNN


0657n          ----------------IKNTNDG--------HTQSQNNKNTQENKAKSLPQTGEESNKDM
0657nHybrid1   ----------------IKNTNDG-------HTQSQNNKNTQENKAKSLPQTGEESNKDM
0657nHybrid2   ----------------IKNTNDG-------HTQSQNNKNTQENKAKSLPQTGEESNKDM
0657nhybrid3   ----------------IKNTNDG-------HTQSQNNKNTQENKAKSLPQTGEESNKDM
ORF0190        TDKVTDKKTTEHLPSDIHKTVDKTVKTKEKAGTPSKENKLSQS---KMLPKTGETTSSQS


0657n          TLPLMALL---ALSSIVAFV-------
0657nHybrid1   TLPLMALL---ALSSIVAFVLPRKRKN
0657nHybrid2   TLPLMALL---ALSSIVAFV-------
0657nhybrid3   TLPLMALL---ALSSIVAFV-------
ORF0190        WWGLYALLGMLALF-IPKFRKESK---
```

Fig. 1C

SEQ ID NO: 8
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFGENIHKYDYTLMVFAQPIYNNPDKFVDEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDSYWKDFMVEGKRVRTISKDPKNNTRTIIFPY
VEGKALYDAIVKVVVKTIDYDGQYHVRIVDKEINTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 11
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 12
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 13
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2A

SEQ ID NO: 14
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALAEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 15
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEDTKKALAEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 16
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTK
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEDTKKALAEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 17
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKKKDGTQQFYHYASSVEPARVIFTK
SKPEIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEDTKKALAEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2B

SEQ ID NO: 18
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEDTKKALAEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 19
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 20
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVKHPIKTGMLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 21
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVKHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2C

SEQ ID NO: 22
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 23
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 24
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYNAEKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 25
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2D

SEQ ID NO: 26
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVVVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 27
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDAKNNTRTIIFPY
VEGKALYDAIVKVVVKTIDYDGQYHVRIVDKEINTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 28
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFNNKEEKYDYTLMVFAQPIYNSADKFKTEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDPKNNTRTIIFPY
VEGKALYDAIVKVVVKTIDYDGQYHVRIVDKEINTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 29
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIIDKDHSAPNWRPIDFEMKNDKGTQQFYHYASSVEPARVIFTK
SKPIIELGLQSGSTWRKFEVYEGDKKLPIKLVSYDTDKDYAYIRFSVSNGTKEVKIVSST
HFGNKEEKYDYTLMVFAQPIYNNPDKFKTEEDYNLQKLLAPYKKAKTLERQVYELEKIQD
KLPEKLKAEYKKKLEQTKKALAEQVKSAITEFQNVQPTNEKMTDLQDAHYVVYESVENSE
SMMDTFVEHPIKTGTLNGKKYMVMKTTNDDYWKDFMVEGKRVRTISKDPKNNTRTIIFPY
VEGKALYDAIVKVVVKTIDYDGQYHVRIVDKEINTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2E

SEQ ID NO: 9
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKEHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKLQE
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTLIFPY
IEGKTLYDAIVKVHVKTIDYEGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 30
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 31
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
IEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 32
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKEHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
IEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2F

SEQ ID NO: 33
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKEHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTLIFPY
IEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 34
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKEHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKLQE
KLPEKLKAEYKKKLEDTKKALDEQVKSAVTEFQNVQPTNDKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTLIFPY
IEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2G

SEQ ID NO: 10
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELRDAIKNPAIKDKEHTAPNSRPIDFEMKKKDGTQQFYHYASTVKPARVIFTD
TKPEIELGLQTAQFWKKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKYKTEEDYKAEKLLAPYKKAKTLERQVYELNKLQD
KLPEKLKAEYKKKLDDTRKALDDQVKSAVTEFQNVQPTNDKLTDLQETKFVVFESVENNE
SVMDTFVKHPIKTAMLNGKKYVVMETTNDDYWKDFIVEGQRVRTVSKDAKNNSRTLIFPY
IEGKTVYDAIVKVHVKTIDYEGQYHVRIIDKDAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 35
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDTVKDYAYIRFSVSNGTKAVKIVSST
HFNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 36
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
SKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 37
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTD
TKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2H

SEQ ID NO: 38
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELREAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASTVKPARVIFTD
TKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 39
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELRDAIKNPAIKDKEHTAPNSRPIDFEMKKKDGTQQFYHYASTVKPARVIFTD
TKPEIELGLQSGQFWRKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKFKTEEDYKAEKLLAPYKKAKTLERQVYELNKIQD
KLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

SEQ ID NO: 40
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVA
SPTTTSEKAPETKPVANAVSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNN
TYPILNQELRDAIKNPAIKDKEHTAPNSRPIDFEMKKKDGTQQFYHYASTVKPARVIFTD
TKPEIELGLQTAQFWRKFEVYEGDKKLPVKLVSYDSVKDYAYIRFSVSNGTRAVKIVSST
HYNNKEEKYDYTLMEFAQPIYNSADKYKTEEDYKAEKLLAPYKKAKTLERQVYELNKLQD
KLPEKLKAEYKKKLDDTKKALDDQVKSAVTEFQNVQPTNEKMTDLQDTKYVVYESVENNE
SMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPY
VEGKTLYDAIVKVHVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQQDNSAKKEATPAT
PSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTT
PTKVVSTTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNK
NTQENKAKSLPQTGEESNKDMTLPLMALLALSSIVAFVLPRKRKN

Fig. 2I

SEQ ID NO: 41
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVASPTTTSEKAPETKPVANA
VSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNNTYPILNQELREAIKNPAIIDKDHSAPNSRPIDFEMK
KKDGTQQFYHYASSVKPARVIFTKTGPVIELGLKTASTWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFPVSNGTRDV
KIVSSIEYGENIHEDYDYTLMVFAQPITNNPDDYVDEETYNLQKLLAPYHKAKTLERQVYELNKIQDKLPEKLKAEYK
KKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDLQDTKYVVFESEENSESVMDGFVEHPFYTATLNGQKYVVMKTKDD
SYWKDLIVEGKRVTTVSKDPKNNSRTIIFPYVEGKAVYNAIVKVVVKTIDYDGQYHVRIVDKEAFTKANTDKSNKKEQ
QDNSAKKEATPATPSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTTPTKVV
STTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNKNTQENKAKSLPQTGEESNKDMTL
PLMALLALSSIVAFV

Fig. 2J

SEQ ID NO: 42
MNKHHPKLRSFYSIRKSTLGVASVIVSTLFLITSQHQAQAAENTNTSDKISENQNNNATTTQQPKDTNQTQPATQPVI
TAKNYPAADESLKDAIKDPALENKEHDIGPREQVNFQLLDKNNETQYYHFFSIKDPADVYYTKKKAEVELDINTASTW
KKFEVYENNQKLPVRLVSYSPVPEDHAYIRFPVSDGTQELKIVSSTQIDDGEETNYDYTKLVFAKPIYNDPSLVKSDT
NDAVVTNDQSSSDASNQTNTNTSNQNTSTTNNANNQPQATTNMSQPAQPKSSANADQASSQPAHETNSNGNTNDKTNE
SSNQSDVNQQYPPADESLQDAIKNPAIKDKDHSAPNSRPIDFEMKKKDGTQQFYHYASSVKPARVIFTDSKPEIELGL
QSGQFWRKFEVYEGDKKLPIKLVSYDTVKDYAYIRFSVSNGTKAVKIVSSTHFNNKEEKYDYTLMEFAQPIYNSADKF
KTEEDYKAEKLLAPYKKAKTLERQVYELNKIQDKLPEKLKAEYKKKLEDTKKALDEQVKSAITEFQNVQPTNEKMTDL
QDTKYVVYESVENNESMMDTFVKHPIKTGMLNGKKYMVMETTNDDYWKDFMVEGQRVRTISKDAKNNTRTIIFPYVEG
KTLYDAIVKVHVKTIDYDGQYHVRIINQDINTKDDDTSQNNTSEPLNVQTGQEGKVADTDVAENSSTATNPKDASDKA
DVIEPESDVVKDADNNIDKDVQHDVDHLSDMSDNNHFDKYDLKEMDTQIAKDTDRNVDNSVGMSSNVDTDKDSNKNKD
KVIQLAHIADKNNHTGKAAKLDVVKQNYNNTDKVTDKKTTEHLPSDIHKTVDKTVKTKEKAGTPSKENKLSQSKMLPK
TGETTSSQSWWGLYALLGMLALFIPKFRKESK

Fig. 2K

SEQ ID NO: 43
MNKQQKEFKSFYSIRKSSLGVASVAISTLLLLMSNGEAQAAAEETGGTNTEAQPKTEAVASPTTTSEKAPETKPVANA
VSVSNKEVEAPTSETKEAKEVKEVKAPKETKEVKPAAKATNNTYPILNQELREAIKNPAIIDKEHTADNWRPIDFQMK
NDKGERQFYHYASTVEPATVIFTKTGPVIELGLKTASTWKKFEVYEGDKKLPVELVSYDSDKDYAYIRFPVSNGTRDV
KIVSSIEYGENIHEDYDYTLMVFAQPITNNPDDYVDEETYNLQKLLAPYHKAKTLERQVYELEKLQEKLPEKYKAEYK
KKLDQTRVELADQVKSAVTEFENVTPTNDQLTDLQEAHFVVFESEENSESVMDGFVEHPFYTATLNGQKYVVMKTKDD
SYWKDLIVEGKRVTTVSKDPKNNSRTLIFPYIPDKAVYNAIVKVVVANIGYEGQYHVRIVDKEAFTKANTDKSNKKEQ
QDNSAKKEATPATPSKPTPSPVEKESQKQDSQKDDNKQLPSVEKENDASSESGKDKTPATKPTKGEVESSSTTPTKVV
STTQNVAKPTTASSKTTKDVVQTSAGSSEAKDSAPLQKANIKNTNDGHTQSQNNKNTQENKAKSLPQTGEESNKDMTL
PLMALLALSSIVAFV

Fig. 2L

a. Forward

```
aac cgg ttt tcc atg ggg aac aaa cag caa aaa gaa ttt
 N   R   F   S   M   G   N   K   Q   Q   K   E   F
```

b. Reverse

```
gta tta cct aga aaa cgt aaa aac ctc gag aaa ccg gt
 V   L   P   R   K   R   K   N  (L   E   K   P)
```

Fig. 3

```
MGNKQQKEFK  SFYSIRKSSL  GVASVAISTL  LLLMSNGEAQ  AAAEETGGTN  TEAQPKTEAV  ASPTTTSEKA
PETKPVANAV  SVSNKEVEAP  TSETKEAKEV  KEVKAPKETK  EVKPAAKATN  NTYPILNQEL  REAIKNPAIK
DKDHSAPNSR  PIDFEMKKKD  GTQQFYHYAS  SVKPARVIFT  DSKPEIELGL  QSGQFWRKFE  VYEGDKKLPI
KLVSYDTVKD  YAYIRFSVSN  GTKAVKIVSS  THFNNKEEKY  DYTLMEFAQP  IYNSADKFKT  EEDYKAEKLL
APYKKAKTLE  RQVYELNKIQ  DKLPEKLKAE  YKKKLEDTKK  ALDEQVKSAI  TEFQNVQPTN  EKMTDLQDTK
YVVYESVENN  ESMMDTFVKH  PIKTGMLNGK  KYMVMETTND  DYWKDFMVEG  QRVRTISKDA  KNNTRTIIFP
YVEGKTLYDA  IVKVHVKTID  YDGQYHVRIV  DKEAFTKANT  DKSNKKEQQD  NSAKKEATPA  TPSKPTPSPV
EKESQKQDSQ  KDDNKQLPSV  EKENDASSES  GKDKTPATKP  TKGEVESSST  TPTKVVSTTQ  NVAKPTTASS
KTTKDVVQTS  AGSSEAKDSA  PLQKANIKNT  NDGHTQSQNN  KNTQENKAKS  LPQTGEESNK  DMTLPLMALL
ALSSIVAFVL  PRKRKNLEHH  HHHH
```

Fig. 4A

```
MN-----/  /----RKRKN*
MGN-----/  /----RKRKNLEHHHHHH*
```

Fig. 4B
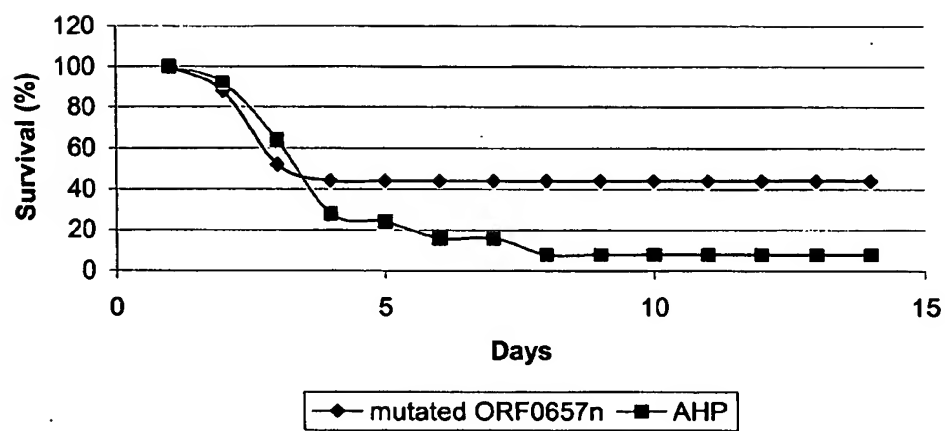
Fig. 5

SEQUENCE LISTING

<110> Anderson, Annaliesa S.
      Kuklin, Nelly
      Jansen, Kathrin Ute

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE
   IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21349PV

<160> 56

<170> FastSEQ for Windows Version 4.0

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<213> Staphylococcus aureus

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 1               5                  10                  15
Ser Thr Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile
            20                  25                  30
Thr Ser Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp
        35                  40                  45
Lys Ile Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro
    50                  55                  60
Lys Asp Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala
65                  70                  75                  80
Lys Asn Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp
            85                  90                  95
Pro Ala Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val
            100                 105                 110
Asn Phe Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe
        115                 120                 125
Phe Ser Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala
    130                     135                 140
Glu Val Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu
145                 150                 155                 160
Val Tyr Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser
            165                 170                 175
Pro Val Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly
            180                 185                 190
Thr Gln Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu
        195                 200                 205
Glu Thr Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr
    210                 215                 220
Asn Asp Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr
225                 230                 235                 240
Asn Asp Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr
            245                 250                 255
Ser Asn Gln Asn Thr Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln
            260                 265                 270
```

-1-

```
Ala Thr Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn
    275             280             285
Ala Asp Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly
    290             295             300
Asn Thr Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn
305             310             315             320
Gln Gln Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn
            325             330             335
Pro Ala Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile
            340             345             350
Asp Phe Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Phe Tyr His Tyr
            355             360             365
Ala Ser Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro
    370             375             380
Ile Ile Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu
385             390             395             400
Val Tyr Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp
            405             410             415
Ser Asp Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr
            420             425             430
Arg Glu Val Lys Ile Val Ser Ser Ile Glu Tyr Gly Glu Asn Ile His
    435             440             445
Glu Asp Tyr Asp Tyr Thr Leu Met Val Phe Ala Gln Pro Ile Thr Asn
    450             455             460
Asn Pro Asp Asp Tyr Val Asp Glu Glu Thr Tyr Asn Leu Gln Lys Leu
465             470             475             480
Leu Ala Pro Tyr His Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu
            485             490             495
Leu Glu Lys Leu Gln Glu Lys Leu Pro Glu Lys Tyr Lys Ala Glu Tyr
            500             505             510
Lys Lys Lys Leu Asp Gln Thr Arg Val Glu Leu Ala Asp Gln Val Lys
    515             520             525
Ser Ala Val Thr Glu Phe Glu Asn Val Thr Pro Thr Asn Asp Gln Leu
    530             535             540
Thr Asp Leu Gln Glu Ala His Phe Val Val Phe Glu Ser Glu Glu Asn
545             550             555             560
Ser Glu Ser Val Met Asp Gly Phe Val Glu His Pro Phe Tyr Thr Ala
            565             570             575
Thr Leu Asn Gly Gln Lys Tyr Val Val Met Lys Thr Lys Asp Asp Ser
            580             585             590
Tyr Trp Lys Asp Leu Ile Val Glu Gly Lys Arg Val Thr Thr Val Ser
    595             600             605
Lys Asp Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro
    610             615             620
Asp Lys Ala Val Tyr Asn Ala Ile Val Lys Val Val Val Ala Asn Ile
625             630             635             640
Gly Tyr Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn
            645             650             655
Thr Lys Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn
            660             665             670
Val Gln Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu
    675             680             685
Asn Ser Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp
    690             695             700
```

```
Val Ile Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile
705             710                 715                     720
Asp Lys Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp
            725                 730                 735
Asn Asn His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile
            740                 745                 750
Ala Lys Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val
            755                 760                 765
Gly Met Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys
    770                 775                 780
Asp Lys Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr
785             790                 795                     800
Gly Lys Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr
            805                 810                 815
Asp Lys Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile
            820                 825                 830
His Lys Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr
        835                 840                 845
Pro Ser Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Pro Lys Thr
    850                 855                 860
Gly Glu Thr Thr Ser Ser Gln Ser Trp Trp Gly Leu Tyr Ala Leu Leu
865                 870                 875                     880
Gly Met Leu Ala Leu Phe Ile Pro Lys Phe Arg Lys Glu Ser Lys
            885                 890                 895
```

<210> 2
<211> 645
<212> PRT
<213> Staphylococcus aureus

<400> 2
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Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
    115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
```

-3-

```
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
                260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
                325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
                340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
                420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
                485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
                500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
                580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
```

-4-

```
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 3
<211> 649
<212> PRT
<213> Staphylococcus aureus

<400> 3
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
                325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
```

-5-

Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355   360   365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370   375   380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385   390   395   400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
          405   410   415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
          420   425   430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
      435   440   445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
      450   455   460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465   470   475   480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
          485   490   495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
          500   505   510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
      515   520   525
Pro Thr Lys Gly Lys Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
      530   535   540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545   550   555   560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
          565   570   575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
          580   585   590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
      595   600   605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
      610   615   620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625   630   635   640
Arg Lys Arg Lys Asn Leu Glu Lys Thr
          645

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<211> 647
<212> PRT
<213> Staphylococcus aureus

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 1   5   10   15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
      20   25   30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
      35   40   45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
      50   55   60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65   70   75   80

```
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
              85                      90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys
             100                     105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
             115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
         130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly
145                 150                 155                     160
Glu Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
             165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
         180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
         195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
         210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                     240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
             245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
             260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
         275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
         290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                     320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
             325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
             340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
         355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
     370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                     400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
             405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
             420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
         435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
     450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                     480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
             485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
             500                 505                 510
```

-7-

```
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val
        530             535             540
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Ala Ser Ser Lys Thr Thr
545             550             555             560
Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp Ser
            565             570             575
Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His Thr
            580             585             590
Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser Leu
            595             600             605
Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu Met
    610             615             620
Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg Lys
625             630             635             640
Arg Lys Asn Leu Glu Lys Pro
            645
```

<210> 5
<211> 645
<212> PRT
<213> Staphylococcus aureus

<400> 5
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
        20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn
        35              40              45
Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr
    50              55              60
Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val
65              70              75              80
Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys
            85              90              95
Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro
        100             105             110
Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
        115             120             125
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
    130             135             140
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu
145             150             155             160
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
            165             170             175
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
            180             185             190
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
        195             200             205
Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
    210             215             220
Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
225             230             235             240
```

```
Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
                 245                 250                 255
Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
             260                 265                 270
Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
         275                 280                 285
Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
     290                 295                 300
Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu
305                 310                 315                 320
Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
                 325                 330                 335
Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
             340                 345                 350
Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
         355                 360                 365
Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
     370                 375                 380
Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg
385                 390                 395                 400
Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile
             405                 410                 415
Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
             420                 425                 430
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
         435                 440                 445
Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys
     450                 455                 460
Glu Gln Gln Asp Asn Ser Ala Lys Arg Glu Ala Thr Pro Ala Thr Pro
465                 470                 475                 480
Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
             485                 490                 495
Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn
             500                 505                 510
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
         515                 520                 525
Ala Lys Gly Glu Val Glu Ser Ser Thr Thr Pro Thr Lys Val Val
     530                 535                 540
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr
545                 550                 555                 560
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
             565                 570                 575
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
             580                 585                 590
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
             595                 600                 605
Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu
     610                 615                 620
Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg
625                 630                 635                 640
Lys Arg Lys Asn Leu
             645
```

<210> 6
<211> 645

-9-

<212> PRT
<213> Staphylococcus aureus

<400> 6

```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr Asn
          35                  40                  45
Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr
    50                  55                  60
Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser Val
65                  70                  75                  80
Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala Lys
              85                  90                  95
Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Ala Val Lys Pro
            100                 105                 110
Ala Thr Lys Ala Asp Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu Leu
          115                 120                 125
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
    130                 135                 140
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Glu Asn Gly Glu
145                 150                 155                 160
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
              165                 170                 175
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
            180                 185                 190
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
    195                 200                 205
Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
    210                 215                 220
Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
225                 230                 235                 240
Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
              245                 250                 255
Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
            260                 265                 270
Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
    275                 280                 285
Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
    290                 295                 300
Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu
305                 310                 315                 320
Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
              325                 330                 335
Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
            340                 345                 350
Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
          355                 360                 365
Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
    370                 375                 380
Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln Arg
385                 390                 395                 400
```

```
Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile
            405             410                 415
Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
            420             425                 430
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
            435             440                 445
Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys Lys
    450             455                 460
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro
465             470                 475                 480
Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
            485             490                 495
Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu Asn
            500             505             ·   510
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
            515             520                 525
Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
            530             535                 540
Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys Thr
545             550                 555                 560
Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
            565             570                 575
Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
            580             585         ·       590
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
            595             600                 605
Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu
    610             615                 620             ·
Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro Arg
625             630                 635                 640
Lys Arg Lys Asn Leu
            645

<210> 7
<211> 654
<212> PRT
<213> Staphylococcus aureus

<400> 7
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1             5                 10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25                  30
Met Ser Asn Gly Glu Ala Lys Ala Ala Glu Glu Thr Gly Gly Thr Ile
            35              40                  45
Thr Glu Thr Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr Thr
    50              55                  60
Thr Glu Lys Ala Pro Glu Ala Lys Pro Val Ala Asn Ala Val Ser Val
65              70                  75                  80
Ser Asn Lys Glu Val Val Ala Pro Thr Thr Glu Thr Lys Glu Ala Lys
            85              90                  95
Glu Val Lys Glu Val Lys Ala Pro Asn Glu Thr Lys Glu Val Lys Pro
            100             105                 110
Ala Ala Lys Ser Asp Asn Asn Thr Tyr Pro Ile Leu Asn Glu Glu Leu
            115             120                 125
```

```
Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser Ala
    130                 135                 140
Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly Thr
145                 150                 155                 160
Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val Ile
                165                 170                 175
Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln
                180                 185                 190
Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile
        195                 200                 205
Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe
        210                 215                 220
Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr His
225                 230                 235                 240
Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala
                245                 250                 255
Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr
                260                 265                 270
Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu
                275                 280                 285
Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys
        290                 295                 300
Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Glu Thr Lys Lys Ala Leu
305                 310                 315                 320
Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln Pro
                325                 330                 335
Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr
                340                 345                 350
Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys His
        355                 360                 365
Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met Glu
    370                 375                 380
Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Glu Arg
385                 390                 395                 400
Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile
                405                 410                 415
Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys Val
                420                 425                 430
His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile Val
        435                 440                 445
Asp Lys Glu Ala Phe Thr Lys Ala Asn Ala Asp Lys Ser Asn Lys Lys
    450                 455                 460
Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr Pro
465                 470                 475                 480
Ser Lys Pro Thr Thr Ala Pro Val Glu Lys Glu Ser Gln Lys Gln Asp
                485                 490                 495
Ser Gln Lys Asp Asp Asn Lys Gln Ser Pro Ser Val Glu Lys Glu Ile
        500                 505                 510
Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys Pro
        515                 520                 525
Ala Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val Val
        530                 535                 540
Ser Ala Thr Gln Asn Val Ala Lys Pro Thr Ser Ala Ser Ser Glu Thr
545                 550                 555                 560
```

- 12 -

```
Thr Lys Gly Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys Asp
             565                     570                 575
Asn Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly His
             580                 585                 590
Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys Ser
         595                 600                 605
Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro Leu
     610                 615                 620
Met Ala Leu Leu Ala Leu Ser Ser Ile Ile Ala Phe Val Leu Pro Arg
625                 630                 635                 640
Lys Arg Lys Asn Leu Glu Lys Pro Val Arg Ala Asn Ser Ser
             645                 650
```

<210> 8
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 8
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1                 5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
             20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
             35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
     50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
             85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
             100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
     115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
     130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
             165                 .170                175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
             180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
             195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
     210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Gly Glu Asn Ile His Lys Tyr Asp Tyr Thr Leu Met Val Phe
             245                 250                 255
```

```
Ala Gln Pro Ile Tyr Asn Asn Pro Asp Lys Phe Val Asp Glu Glu Asp
            260                 265             270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275             280             285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
        290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305             310             315             320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340             345             350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355             360             365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Lys Thr Thr Asn Asp Ser Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Pro Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435             440             445
Val Asp Lys Glu Ile Asn Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645

<210> 9
<211> 645
<212> PRT
<213> Artificial Sequence
```

- 14 -

```
<220>
<223> Hybrid sequence

<400> 9
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Val Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Leu Gln Glu Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
                325                 330                 335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
```

- 15 -

```
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Leu
            405             410             415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Glu Gly Gln Tyr His Val Arg Ile
            435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
        450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
            530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645
```

```
<210> 10
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 10
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
```

-16-

```
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                     105                     110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                     120                     125
Leu Arg Asp Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Thr
        130                     135                     140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                     150                     155                     160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Thr Val Lys Pro Ala Arg Val
                165                     170                     175
Ile Phe Thr Asp Thr Lys Pro Glu Ile Glu Leu Gly Leu Gln Thr Ala
            180                     185                     190
Gln Phe Trp Lys Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                     200                     205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
        210                     215                     220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225                     230                     235                     240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                     250                     255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Tyr Lys Thr Glu Glu Asp
            260                     265                     270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                     280                     285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Leu Gln Asp Lys Leu Pro Glu
        290                     295                     300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Asp Asp Thr Arg Lys Ala
305                     310                     315                     320
Leu Asp Asp Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325                     330                     335
Pro Thr Asn Asp Lys Leu Thr Asp Leu Gln Glu Thr Lys Phe Val Val
        340                     345                     350
Phe Glu Ser Val Glu Asn Asn Glu Ser Val Met Asp Thr Phe Val Lys
        355                     360                     365
His Pro Ile Lys Thr Ala Met Leu Asn Gly Lys Lys Tyr Val Val Met
        370                     375                     380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Ile Val Glu Gly Gln
385·                    390                     395                     400
Arg Val Arg Thr Val Ser Lys Asp Ala Lys Asn Asn Ser Arg Thr Leu
                405                     410                     415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Val Tyr Asp Ala Ile Val Lys
            420                     425                     430
Val His Val Lys Thr Ile Asp Tyr Glu Gly Gln Tyr His Val Arg Ile
        435                     440                     445
Ile Asp Lys Asp Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
        450                     455                     460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                     470                     475                     480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
                485                     490                     495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                     505                     510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515                     520                     525
```

-17-

```
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550             555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
        .   565             570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635                 640
Arg Lys Arg Lys Asn
            . 645
```

<210> 11
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 11
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1                 5               10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
        20          .       25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75                  80'
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr.Lys Glu Ala
            85          .       90      .           95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
    115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130             135             140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150             155             .   160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165             170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180             185             190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
```

```
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225               230               235                   240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
              245               250               255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
          260               265               270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
      275               280               285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
      290               295               300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305               310               315                   320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
              325               330               335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
          340               345               350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
      355               360               365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
      370               375               380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385               390               395                   400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
              405               410               415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
          420               425               430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
      435               440               445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
      450               455               460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465               470               475                   480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
          485               490               495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
          500               505               510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
      515               520               525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
      530               535               540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545               550               555                   560
Thr Thr Lys Asp Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
          565               570               575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
          580               585               590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
      595               600               605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
      610               615               620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625               630               635                   640
Arg Lys Arg Lys Asn
              645
```

```
<210> 12
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 12
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
                260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
                325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
            355                 360                 365
```

```
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
        500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
        580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645
```

```
<210> 13
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 13
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
```

```
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70                  75                      80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                     160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                     240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
        260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                     320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                     400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                     480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
```

```
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
            530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
            610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645


<210> 14
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 14
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
            50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
            130             135             140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150             155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165             170             175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180             185             190
```

```
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225             230             235             240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245             250             255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260             265             270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275             280             285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305             310             315             320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
```

```
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 15
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 15
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
```

-25-

```
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
                325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
                340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
            355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
        370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
                485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
                645
```

<210> 16
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 16
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1             5              10              15
```

```
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Asn Ala Val Ser
    50              55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
            245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
```

- 27 -

```
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
450                     455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                     480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
                485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                     560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                     640
Arg Lys Arg Lys Asn
                645

<210> 17
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 17
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                      80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
```

```
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
        180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
        500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
```

-29.-

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```
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 18
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 18
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1                 5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala.Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
```

```
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275             280             285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
        290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305             310             315             320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
        370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
        420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
        450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
        530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
        580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
        610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645
```

<210> 19
<211> 645
<212> PRT
<213> Artificial Sequence

<220>

<223> Hybrid sequence

<400> 19

```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
        340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
```

```
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
                645


<210> 20
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 20
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1           5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105             110
```

-33-

```
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
    115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Lys
    355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
    500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
```

- 34 -

```
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645


<210> 21
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 21
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
        20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
        100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
    115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130             135             140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145             150             155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165             170             175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
        180             185             190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225             230             235             240
```

```
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
        290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
370                 375                 380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
        450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
        530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
            645
```

<210> 22
<211> 645

<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 22
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
    355                 360                 365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
```

- 37 -

```
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405             410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420             425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630                 635                 640
Arg Lys Arg Lys Asn
                645
```

<210> 23
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 23
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1           5               10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70                  75                  80
```

-38-

```
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                      90                      95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                     105                     110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                     120                     125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130                     135                     140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                     150                     155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                     170                     175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                     185                     190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                     200                     205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                     215                     220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                     230                     235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                     250                     255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                     265                     270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                     280                     285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                     295                     300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                     310                     315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                     330                     335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340                     345                     350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
    355                     360                     365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370                     375                     380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                     390                     395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405                     410                     415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420                     425                     430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435                     440                     445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                     455                     460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                     470                     475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                     490                     495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                     505                     510
```

```
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
        530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
                580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
        610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645

<210> 24
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 24
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
        50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
        130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
```

-40-

```
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210               215               220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225               230               235               240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
             ·245               250               255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260               265               270
Tyr Asn Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275               280               285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290               295               300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305               310               315               320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325               330               ·335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
        340               345               350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355               360               365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370               375               380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385               390               395               400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405               410               415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420               425               430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435               440               445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450               455               460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465               470               475               480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485               490               495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500               505               510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515               520               525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530               535               540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545               550               555               560
Thr Thr Lys Asp Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565               570               575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
        580               585               590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595               600               605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610               615               620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625               630               635               640
```

```
Arg Lys Arg Lys Asn
                645

<210> 25
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 25
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
             20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
         35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
     50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
                260                 265                 270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
            275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
                325                 330                 335
```

-42-

```
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
            355                 360                 365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
        370                 375                 380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645
```

```
<210> 26
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 26
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
```

```
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
        50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130             135             140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145             150.            155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165             170             175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180             185             190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225             230             235             240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245             250             255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260             265             270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275             280             285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305             310             315             320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
        340             345             350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355             360             365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
        420             425             430
Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
```

```
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             .590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645

<210> 27
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 27
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1           5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130             135             140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145             150             155             160
```

```
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
            165             170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180             185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225             230             235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
            245             250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260             265             270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275             280             285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305             310             315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
            340             345             350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355             360             365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385             390             395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
        420             425             430
Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ile Asn Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585                 590
```

- -46 -

```
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 28
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 28
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70           ·           75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145   ·             150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210         ·       215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
```

- 47 -

```
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305             310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
        340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355                 360                 365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Pro Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
        420                 425                 430
Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ile Asn Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645
```

<210> 29
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

-48-

```
<400> 29
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Trp Arg Pro Ile Asp Phe Glu Met Lys Asn Asp Lys Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Glu Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Ser Lys Pro Ile Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Asp Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Glu Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Gly Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Val Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Asn Pro Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Glu Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Gln Thr Lys Lys Ala
305                 310                 315                 320
Leu Ala Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Ala His Tyr Val Val
        340                 345                 350
Tyr Glu Ser Val Glu Asn Ser Glu Ser Met Met Asp Thr Phe Val Glu
        355                 360                 365
His Pro Ile Lys Thr Gly Thr Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Lys Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Lys
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Pro Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Ala Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
```

```
Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ile Asn Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
     450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
             485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
         500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
         515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
     530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
             565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
         580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
     595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
     610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
             645

<210> 30
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 30
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1                 5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
             20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
         35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
     50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
             85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
         100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
     115                 120         .           125
```

-50-

```
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130             135             140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150             155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165             170             175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
        180             185             190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200             205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225             230             235             240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
            245             250             255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260             265             270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275             280             285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305             310             315             320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
        420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
        500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
```

-51-

```
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
        610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 31
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 31
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20          .       25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
        130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
        210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
```

```
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu .
        275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
        290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln .
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
        515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545 .               550                 555                 560
Thr Thr Lys Asp Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
        580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
            645
```

<210> 32
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 32

```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
 1           5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Val Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
            355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
```

-54-

```
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
            435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
            530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
            610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
            645

<210> 33
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 33
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
        50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
```

```
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195                 200                 205
Val Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Leu
            405                 410                 415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
        500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
```

- 56 -

```
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645
```

```
<210> 34
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 34
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10              15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75              80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95·
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
        100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Ser
    130             135             140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150             155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165             170             175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180             185             190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200             205
Val Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
 . 210             215             220
```

```
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225               ·   230               235               240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
              245               250               255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
          260               265               270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275               280       ·       285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Leu Gln Glu Lys Leu Pro Glu
    290               295               300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305               310               315               320
Leu Asp Glu Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
              325               330               335
Pro Thr Asn Asp Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
          340               345               350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355               360               365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370               375               380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385               390               395               400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Leu
          405               410               415
Ile Phe Pro Tyr Ile Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
          420               425               430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435               440               445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450               455               460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465               470               475               480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
              485               490               495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
          500               505               510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
          515       ·       520               525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530               535               540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545               550               555               560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
              565               570               575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
          580               585               590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
          595               600               605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610               615               620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625               630               635               640
Arg Lys Arg Lys Asn
              645
```

```
<210> 35
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 35
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
        180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195                 200                 205
Val Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355                 360                 365
```

-59-

```
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
                405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
        435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    .515                520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
        595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 36
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 36
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                 10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
```

```
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
                100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
            165                 170                 175
Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                 240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300  .
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                 320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355                 360  .                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                 400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 .   495
```

- 61 -

```
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
            530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
            610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645
```

<210> 37
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 37
```
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1                   5                   10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
            50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
            130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Asp Thr Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180                 185                 190
```

- 62 -

```
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195                     200             205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225                 230                 235                     240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245                 250                     255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260                 265             270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275                 280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290                 295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305                 310                 315                     320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325                 330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340                 345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355                 360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370                 375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385                 390                 395                     400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405                 410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420                 425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435                 440                 445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                     480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                     560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
                565                 570                     575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
```

```
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 38
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 38
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1                 5                 10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
          20                25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35                40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
              85                90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
          100               105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
          115               120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His Ser
    130               135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145               150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Thr Val Lys Pro Ala Arg Val
              165               170                 175
Ile Phe Thr Asp Thr Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
              180               185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195               200                 205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
    210               215                 220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225               230                 235                 240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
              245               250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
          260               265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275               280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290               295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305               310                 315                 320
```

```
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
            340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
            355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
            420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
            515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
            530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580             585             590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595             600             605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610             615             620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625             630             635             640
Arg Lys Arg Lys Asn
            645

<210> 39
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 39
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1             5              10              15
```

- 65 -

```
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
        20              25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70                  75                      80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
                85              90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100             105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115             120                 125
Leu Arg Asp Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Thr
    130             135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150                 155                     160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Thr Val Lys Pro Ala Arg Val
                165             170                 175
Ile Phe Thr Asp Thr Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser Gly
            180             185                 190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
        195             200                 205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
    210             215                 220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225             230                 235                     240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
                245             250                 255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu Asp
            260             265                 270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
        275             280                 285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro Glu
    290             295                 300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys Ala
305             310                 315                     320
Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val Gln
            325             330                 335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340             345                 350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
        355             360                 365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375                 380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390                 395                     400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410                 415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
        420             425                 430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435             440                 445
```

-66-

```
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450                 455                 460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465                 470                 475                 480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485                 490                 495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
            500                 505                 510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515                 520                 525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530                 535                 540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545                 550                 555                 560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565                 570                 575
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
    595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645


<210> 40
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 40
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1                 5                 10                15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                25                30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                40                45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                55                60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                70                75                80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                90                95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100               105               110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
    115               120               125
Leu Arg Asp Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Glu His Thr
    130               135               140
```

```
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145             150             155             160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Thr Val Lys Pro Ala Arg Val
            165             170             175
Ile Phe Thr Asp Thr Lys Pro Glu Ile Glu Leu Gly Leu Gln Thr Ala
        180             185             190
Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195             200             205
Val Lys Leu Val Ser Tyr Asp Ser Val Lys Asp Tyr Ala Tyr Ile Arg
    210             215             220
Phe Ser Val Ser Asn Gly Thr Arg Ala Val Lys Ile Val Ser Ser Thr
225             230             235             240
His Tyr Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu Phe
            245             250             255
Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Tyr Lys Thr Glu Glu Asp
        260             265             270
Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr Leu
    275             280             285
Glu Arg Gln Val Tyr Glu Leu Asn Lys Leu Gln Asp Lys Leu Pro Glu
    290             295             300
Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Asp Asp Thr Lys Lys Ala
305             310             315             320
Leu Asp Asp Gln Val Lys Ser Ala Val Thr Glu Phe Gln Asn Val Gln
            325             330             335
Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val Val
        340             345             350
Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val Lys
    355             360             365
His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val Met
    370             375             380
Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly Gln
385             390             395             400
Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr Ile
            405             410             415
Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val Lys
        420             425             430
Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg Ile
    435             440             445
Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn Lys
    450             455             460
Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala Thr
465             470             475             480
Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys Gln
            485             490             495
Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys Glu
        500             505             510
Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr Lys
    515             520             525
Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys Val
    530             535             540
Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser Lys
545             550             555             560
Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala Lys
            565             570             575
```

-68-

```
Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp Gly
            580                 585                 590
His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala Lys
            595                 600                 605
Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu Pro
    610                 615                 620
Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro
625                 630                 635                 640
Arg Lys Arg Lys Asn
                645
```

```
<210> 41
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 41
Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
  1               5                  10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20                  25                  30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
            35                  40                  45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50                  55                  60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65                  70                  75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85                  90                  95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
            100                 105                 110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
            115                 120                 125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Asp His Ser
    130                 135                 140
Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp Gly
145                 150                 155                 160
Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg Val
                165                 170                 175
Ile Phe Thr Lys Thr Gly Pro Val Ile Glu Leu Gly Leu Lys Thr Ala
            180                 185                 190
Ser Thr Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
            195                 200                 205
Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile Arg
    210                 215                 220
Phe Pro Val Ser Asn Gly Thr Arg Asp Val Lys Ile Val Ser Ser Ile
225                 230                 235                 240
Glu Tyr Gly Glu Asn Ile His Glu Asp Tyr Asp Tyr Thr Leu Met Val
                245                 250                 255
Phe Ala Gln Pro Ile Thr Asn Asn Pro Asp Asp Tyr Val Asp Glu Glu
            260                 265                 270
```

```
Thr Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr His Lys Ala Lys Thr
        275             280             285
Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro
    290             295                 300
Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys
305             310                 315                 320
Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val
            325             330                 335
Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val
            340             345                 350
Val Phe Glu Ser Glu Glu Asn Ser Glu Ser Val Met Asp Gly Phe Val
        355             360             365
Glu His Pro Phe Tyr Thr Ala Thr Leu Asn Gly Gln Lys Tyr Val Val
    370             375             380
Met Lys Thr Lys Asp Asp Ser Tyr Trp Lys Asp Leu Ile Val Glu Gly
385             390                 395                 400
Lys Arg Val Thr Thr Val Ser Lys Asp Pro Lys Asn Asn Ser Arg Thr
            405             410                 415
Ile Ile Phe Pro Tyr Val Glu Gly Lys Ala Val Tyr Asn Ala Ile Val
            420             425             430
Lys Val Val Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg
        435             440             445
Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn
    450             455             460
Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala
465             470                 475                 480
Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys
            485             490                 495
Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys
            500             505             510
Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr
            515             520             525
Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys
    530             535             540
Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser
545             550             555             560
Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala
            565             570             575
Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp
            580             585             590
Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala
        595             600             605
Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu
    610             615             620
Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val
625             630             635
```

<210> 42
<211> 890
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

```
<400> 42
Met Asn Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys
1               5                   10                  15
Ser Thr Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile
            20                  25                  30
Thr Ser Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp
        35                  40                  45
Lys Ile Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Gln Pro
    50                  55                  60
Lys Asp Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Val Ile Thr Ala
65              70                  75                  80
Lys Asn Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp
            85                  90                  95
Pro Ala Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val
            100                 105                 110
Asn Phe Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe
        115                 120                 125
Phe Ser Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala
    130                 135                 140
Glu Val Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu
145                 150                 155                 160
Val Tyr Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser
            165                 170                 175
Pro Val Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly
            180                 185                 190
Thr Gln Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu
        195                 200                 205
Glu Thr Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr
    210                 215                 220
Asn Asp Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr
225                 230                 235                 240
Asn Asp Gln Ser Ser Ser Asp Ala Ser Asn Gln Thr Asn Thr Asn Thr
            245                 250                 255
Ser Asn Gln Asn Thr Ser Thr Thr Asn Asn Ala Asn Asn Gln Pro Gln
            260                 265                 270
Ala Thr Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Ala Asn
        275                 280                 285
Ala Asp Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly
    290                 295                 300
Asn Thr Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn
305                 310                 315                 320
Gln Gln Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn
            325                 330                 335
Pro Ala Ile Lys Asp Lys Asp His Ser Ala Pro Asn Ser Arg Pro Ile
        340                 345                 350
Asp Phe Glu Met Lys Lys Lys Asp Gly Thr Gln Gln Phe Tyr His Tyr
        355                 360                 365
Ala Ser Ser Val Lys Pro Ala Arg Val Ile Phe Thr Asp Ser Lys Pro
    370                 375                 380
Glu Ile Glu Leu Gly Leu Gln Ser Gly Gln Phe Trp Arg Lys Phe Glu
385                 390                 395                 400
Val Tyr Glu Gly Asp Lys Lys Leu Pro Ile Lys Leu Val Ser Tyr Asp
            405                 410                 415
Thr Val Lys Asp Tyr Ala Tyr Ile Arg Phe Ser Val Ser Asn Gly Thr
            420                 425                 430
```

-71-

```
Lys Ala Val Lys Ile Val Ser Ser Thr His Phe Asn Asn Lys Glu Glu
        435             440                 445
Lys Tyr Asp Tyr Thr Leu Met Glu Phe Ala Gln Pro Ile Tyr Asn Ser
    450             455                 460
Ala Asp Lys Phe Lys Thr Glu Glu Asp Tyr Lys Ala Glu Lys Leu Leu
465             470                 475                 480
Ala Pro Tyr Lys Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu
            485                 490                 495
Asn Lys Ile Gln Asp Lys Leu Pro Glu Lys Leu Lys Ala Glu Tyr Lys
        500                 505                 510
Lys Lys Leu Glu Asp Thr Lys Lys Ala Leu Asp Glu Gln Val Lys Ser
        515                 520                 525
Ala Ile Thr Glu Phe Gln Asn Val Gln Pro Thr Asn Glu Lys Met Thr
        530                 535                 540
Asp Leu Gln Asp Thr Lys Tyr Val Val Tyr Glu Ser Val Glu Asn Asn
545             550                 555                 560
Glu Ser Met Met Asp Thr Phe Val Lys His Pro Ile Lys Thr Gly Met
            565                 570                 575
Leu Asn Gly Lys Lys Tyr Met Val Met Glu Thr Thr Asn Asp Asp Tyr
        580                 585                 590
Trp Lys Asp Phe Met Val Glu Gly Gln Arg Val Arg Thr Ile Ser Lys
    595             600                 605
Asp Ala Lys Asn Asn Thr Arg Thr Ile Ile Phe Pro Tyr Val Glu Gly
    610             615                 620
Lys Thr Leu Tyr Asp Ala Ile Val Lys Val His Val Lys Thr Ile Asp
625             630                 635                 640
Tyr Asp Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn Thr
            645                 650                 655
Lys Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn Val
        660                 665                 670
Gln Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu Asn
    675                 680                 685
Ser Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp Val
    690                 695                 700
Ile Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile Asp
705             710                 715                 720
Lys Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp Asn
            725                 730                 735
Asn His Phe Asp Lys Tyr Asp Leu Lys Glu Met Asp Thr Gln Ile Ala
        740                 745                 750
Lys Asp Thr Asp Arg Asn Val Asp Asn Ser Val Gly Met Ser Ser Asn
    755                 760                 765
Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys Val Ile Gln
    770                 775                 780
Leu Ala His Ile Ala Asp Lys Asn Asn His Thr Gly Lys Ala Ala Lys
785             790                 795                 800
Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys Val Thr Asp
            805                 810                 815
Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys Thr Val Asp
        820                 825                 830
Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser Lys Glu Asn
        835                 840                 845
Lys Leu Ser Gln Ser Lys Met Leu Pro Lys Thr Gly Glu Thr Thr Ser
    850                 855                 860
```

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Ser Gln Ser Trp Trp Gly Leu Tyr Ala Leu Leu Gly Met Leu Ala Leu
865               870              ·875                 880
Phe Ile Pro Lys Phe Arg Lys Glu Ser Lys .
                885             890
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<210> 43
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Hybrid sequence

<400> 43
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Met Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg Lys
1               5               10                  15
Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu Leu
            20              25              30
Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly Thr
        35              40              45
Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr Thr
    50              55              60
Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val Ser
65              70              75                  80
Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu Ala
            85              90              95
Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val Lys
        100             105             110
Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln Glu
        115             120             125
Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Ile Asp Lys Glu His Thr
    130             135             140
Ala Asp Asn Trp Arg Pro Ile Asp Phe Gln Met Lys Asn Asp Lys Gly
145             150             155                 160
Glu Arg Gln Phe Tyr His Tyr Ala Ser Thr Val Glu Pro Ala Thr Val
            165             170                 175
Ile Phe Thr Lys Thr Gly Pro Val Ile Glu Leu Gly Leu Lys Thr Ala
        180             185                 190
Ser Thr Trp Lys Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu Pro
    195             200                 205
Val Glu Leu Val Ser Tyr Asp Ser Asp Lys Asp Tyr Ala Tyr Ile Arg
    210             .215                220
Phe Pro Val Ser Asn Gly Thr Arg Asp Val Lys Ile Val Ser Ser Ile
225             230             235                 240
Glu Tyr Gly Glu Asn Ile His Glu Asp Tyr Asp Tyr Thr Leu Met Val
            245             250             255
Phe Ala Gln Pro Ile Thr Asn Asn Pro Asp Asp Tyr Val Asp Glu Glu
            260             265             270
Thr Tyr Asn Leu Gln Lys Leu Leu Ala Pro Tyr His Lys Ala Lys Thr
            275             280             285
Leu Glu Arg Gln Val Tyr Glu Leu Glu Lys Leu Gln Glu Lys Leu Pro
        290             295             300
Glu Lys Tyr Lys Ala Glu Tyr Lys Lys Lys Leu Asp Gln Thr Arg Val
305             310             315                 320
```

-73-

```
Glu Leu Ala Asp Gln Val Lys Ser Ala Val Thr Glu Phe Glu Asn Val
            325             330             335
Thr Pro Thr Asn Asp Gln Leu Thr Asp Leu Gln Glu Ala His Phe Val
            340             345             350
Val Phe Glu Ser Glu Glu Asn Ser Glu Ser Val Met Asp Gly Phe Val
            355             360             365
Glu His Pro Phe Tyr Thr Ala Thr Leu Asn Gly Gln Lys Tyr Val Val
        370             375             380
Met Lys Thr Lys Asp Asp Ser Tyr Trp Lys Asp Leu Ile Val Glu Gly
385             390             395             400
Lys Arg Val Thr Thr Val Ser Lys Asp Pro Lys Asn Asn Ser Arg Thr
            405             410             415
Leu Ile Phe Pro Tyr Ile Pro Asp Lys Ala Val Tyr Asn Ala Ile Val
            420             425             430
Lys Val Val Val Ala Asn Ile Gly Tyr Glu Gly Gln Tyr His Val Arg
        435             440             445
Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn
    450             455             460
Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala
465             470             475             480
Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys
            485             490             495
Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys
            500             505             510
Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr
        515             520             525
Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys
        530             535             540
Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser
545             550             555             560
Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala
            565             570             575
Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp
        580             585             590
Gly His Thr Gln Ser Gln Asn Lys Asn Thr Gln Glu Asn Lys Ala
        595             600             605
Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu
    610             615             620
Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val
625             630             635

<210> 44
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> 0657 mutated protein

<400> 44
Met Gly Asn Lys Gln Gln Lys Glu Phe Lys Ser Phe Tyr Ser Ile Arg
 1           5              10              15
Lys Ser Ser Leu Gly Val Ala Ser Val Ala Ile Ser Thr Leu Leu Leu
        20              25              30
```

-74-

```
Leu Met Ser Asn Gly Glu Ala Gln Ala Ala Ala Glu Glu Thr Gly Gly
        35                  40                  45
Thr Asn Thr Glu Ala Gln Pro Lys Thr Glu Ala Val Ala Ser Pro Thr
        50                  55                  60
Thr Thr Ser Glu Lys Ala Pro Glu Thr Lys Pro Val Ala Asn Ala Val
65                  70                  75                  80
Ser Val Ser Asn Lys Glu Val Glu Ala Pro Thr Ser Glu Thr Lys Glu
                85                  90                  95
Ala Lys Glu Val Lys Glu Val Lys Ala Pro Lys Glu Thr Lys Glu Val
                100                 105                 110
Lys Pro Ala Ala Lys Ala Thr Asn Asn Thr Tyr Pro Ile Leu Asn Gln
        115                 120                 125
Glu Leu Arg Glu Ala Ile Lys Asn Pro Ala Ile Lys Asp Lys Asp His
        130                 135                 140
Ser Ala Pro Asn Ser Arg Pro Ile Asp Phe Glu Met Lys Lys Lys Asp
145                 150                 155                 160
Gly Thr Gln Gln Phe Tyr His Tyr Ala Ser Ser Val Lys Pro Ala Arg
                165                 170                 175
Val Ile Phe Thr Asp Ser Lys Pro Glu Ile Glu Leu Gly Leu Gln Ser
                180                 185                 190
Gly Gln Phe Trp Arg Lys Phe Glu Val Tyr Glu Gly Asp Lys Lys Leu
        195                 200                 205
Pro Ile Lys Leu Val Ser Tyr Asp Thr Val Lys Asp Tyr Ala Tyr Ile
        210                 215                 220
Arg Phe Ser Val Ser Asn Gly Thr Lys Ala Val Lys Ile Val Ser Ser
225                 230                 235                 240
Thr His Phe Asn Asn Lys Glu Glu Lys Tyr Asp Tyr Thr Leu Met Glu
                245                 250                 255
Phe Ala Gln Pro Ile Tyr Asn Ser Ala Asp Lys Phe Lys Thr Glu Glu
                260                 265                 270
Asp Tyr Lys Ala Glu Lys Leu Leu Ala Pro Tyr Lys Lys Ala Lys Thr
        275                 280                 285
Leu Glu Arg Gln Val Tyr Glu Leu Asn Lys Ile Gln Asp Lys Leu Pro
        290                 295                 300
Glu Lys Leu Lys Ala Glu Tyr Lys Lys Lys Leu Glu Asp Thr Lys Lys
305                 310                 315                 320
Ala Leu Asp Glu Gln Val Lys Ser Ala Ile Thr Glu Phe Gln Asn Val
                325                 330                 335
Gln Pro Thr Asn Glu Lys Met Thr Asp Leu Gln Asp Thr Lys Tyr Val
                340                 345                 350
Val Tyr Glu Ser Val Glu Asn Asn Glu Ser Met Met Asp Thr Phe Val
        355                 360                 365
Lys His Pro Ile Lys Thr Gly Met Leu Asn Gly Lys Lys Tyr Met Val
        370                 375                 380
Met Glu Thr Thr Asn Asp Asp Tyr Trp Lys Asp Phe Met Val Glu Gly
385                 390                 395                 400
Gln Arg Val Arg Thr Ile Ser Lys Asp Ala Lys Asn Asn Thr Arg Thr
                405                 410                 415
Ile Ile Phe Pro Tyr Val Glu Gly Lys Thr Leu Tyr Asp Ala Ile Val
                420                 425                 430
Lys Val His Val Lys Thr Ile Asp Tyr Asp Gly Gln Tyr His Val Arg
        435                 440                 445
Ile Val Asp Lys Glu Ala Phe Thr Lys Ala Asn Thr Asp Lys Ser Asn
        450                 455                 460
```

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Lys Lys Glu Gln Gln Asp Asn Ser Ala Lys Lys Glu Ala Thr Pro Ala
465             470             475             480
Thr Pro Ser Lys Pro Thr Pro Ser Pro Val Glu Lys Glu Ser Gln Lys
            485             490                 495
Gln Asp Ser Gln Lys Asp Asp Asn Lys Gln Leu Pro Ser Val Glu Lys
            500             505             510
Glu Asn Asp Ala Ser Ser Glu Ser Gly Lys Asp Lys Thr Pro Ala Thr
            515         .       520             525
Lys Pro Thr Lys Gly Glu Val Glu Ser Ser Ser Thr Thr Pro Thr Lys
    530             535             540
Val Val Ser Thr Thr Gln Asn Val Ala Lys Pro Thr Thr Ala Ser Ser
545             550             555             560
Lys Thr Thr Lys Asp Val Val Gln Thr Ser Ala Gly Ser Ser Glu Ala
            565             570             575
Lys Asp Ser Ala Pro Leu Gln Lys Ala Asn Ile Lys Asn Thr Asn Asp
            580             585             590
Gly His Thr Gln Ser Gln Asn Asn Lys Asn Thr Gln Glu Asn Lys Ala
        595             600             605
Lys Ser Leu Pro Gln Thr Gly Glu Glu Ser Asn Lys Asp Met Thr Leu
    610             615             620
Pro Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu
625             630             635             640
Pro Arg Lys Arg Lys Asn Leu Glu His His His His His His
            645             650     .
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<210> 45
<211> 1938
<212> DNA
<213> Artificial Sequence

<220>
<223> 0657 cDNA

<400> 45
atgaacaaac agcaaaaaga atttaaatca ttttattcaa ttagaaagtc atcactaggc 60
gttgcatctg tagcaattag tacacttta ttattaatgt caaatggcga agcacaagca 120
gcagctgaag aaacaggtgg tacaaataca gaagcacaac caaaaactga agcagttgca 180
agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240
gtatctaata aagaagttga ggccctact tctgaaacaa aagaagctaa agaagttaaa 300
gaagttaaag cccctaagga aacaaaagaa gttaaaccag cagcaaaagc cactaacaat 360
acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagac 420
aaagatcata gcgcaccaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480
actcaacagt tttatcatta tgcaagttct gttaaacctg ctagagttat tttcactgat 540
tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600
tatgaaggtg acaaaaagtt gccaattaaa ttagtatcat acgatactgt taaagattat 660
gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720
cacttcaata acaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780
tataacagtg cagataaatt caaaactgaa gaagattata agctgaaaa attattagcg 840
ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900
aaacttcctg aaaaattaaa ggctgagtac aagaagaaat tagaggatac aaagaaagct 960
ttagatgagc aagtgaaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020
aaaatgactg atttacaaga tacaaaatat gttgtttatg aaagtgttga gaataacgaa 1080
tctatgatgg atactttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140
tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200
cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260
```

```
gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320
gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380
aaatctaaca aaaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440
cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500
gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560
aaagacaaaa cgcctgctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620
ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatcaaaa 1680
acaacaaaag atgttgttca aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740
ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800
aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860
atgacattac cattaatggc attattagct ttaagtagca tcgttgcatt cgtattacct 1920
agaaaacgta aaaactaa                                                1938
```

<210> 46
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657nF primer

<400> 46
aaccggtttt ccatggggaa caaacagcaa aaagaattt   39

<210> 47
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657n encoded amino acid

<400> 47
Asn Arg Phe Ser Met Gly Asn Lys Gln Gln Lys Glu
 1   5   10

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> ORF0657nR primer sequence

<400> 48
gtattaccta gaaaacgtaa aaacctcgag aaaccggt   38

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> ORF0657nR encoded amino acid

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<400> 49
Val Leu Pro Arg Lys Arg Lys Asn Leu Glu Lys Pro
 1               5               10

<210> 50
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> M13F

<400> 50
ctggccgtcg ttttac                                                  16

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> M13R

<400> 51
caggaaacag ctatgac                                                 17

<210> 52
<211> 1938
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA encoding ORF0657n protein of SEQ 3

<400> 52
atgaacaaac agcaaaaaga atttaaatca ttttattcaa ttagaaagtc atcactaggc 60
gttgcatctg tagcaattag tacactttta ttattaatgt caaatggcga agcacaagca 120
gcagctgaag aaacaggtgg tacaaataca gaagcacaac caaaaactga agcagttgca 180
agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240
gtatctaata agaagttga ggctcctact tctgaaacaa aagaagctaa agaagttaaa 300
gaagttaaag cccctaagga aacaaaagaa gttaaaccag cagcaaaagc cactaacaat 360
acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagac 420
aaagatcata gcgcaccaaa ctctcgtcca attgattttg aaatgaaaaa gaaagatgga 480
actcaacagt tttatcatta tgcaagttct gttaaacctg ctagagttat tttcactgat 540
tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600
tatgaaggtg acaaaaagtt gccaattaaa ttagtatcat acgatactgt taaagattat 660
gcttacattc gcttctctgt atcaaacgga acaaaagctg ttaaaattgt tagttcaaca 720
cacttcaata acaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780
tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840
ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900
aaacttcctg aaaaattaaa ggctgagtac aagaagaaat tagaggatac aaagaaagct 960
ttagatgagc aagtgaaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020
aaaatgactg atttacaaga tacaaaatat gttgtttatg aaagtgttga gaataacgaa 1080
tctatgatgg atactttgt taaacaccct attaaaacag gtatgcttaa cggcaaaaaa 1140
tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200
```

```
cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260
gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320
gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380
aaatctaaca aaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440
cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500
gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560
aaagacaaaa cgcctgctac aaaaccaact aaaggtaaag tagaatcaag tagtacaact 1620
ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatcaaaa 1680
acaacaaaag atgttgttca aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740
ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800
aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860
atgacattac cattaatggc attattagct ttaagtagca tcgttgcatt cgtattacct 1920
agaaaacgta aaaactaa                                                  1938
```

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<210> 53
<211> 1938
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA encoding ORF0657n protein of SEQ 4

<400> 53
atgaacaaac agcaaaaaga atttaaatca ttttattcaa ttagaaagtc atcactaggc 60
gttgcatctg tagcgattag tacactttta ttattaatgt caaatggcga agcacaagca 120
gcagctgaag aaacaggtgg tacaaataca gaagcacaac caaaaactga agcagttgca 180
agtccaacaa caacatctga aaaagctcca gaaactaaac cagtagctaa tgctgtctca 240
gtatctaata agaagttga ggcccctact tctgaaacaa aagaagctaa agaagttaaa 300
gaagttaaag cccctaagga aacaaaagca gttaaaccag cagcaaaagc cactaacaat 360
acatatccta ttttgaatca ggaacttaga gaagcgatta aaaaccctgc aataaaagat 420
aaagatcata gcgcaccaaa ctctcgtcca attgattttg aaatgaaaaa agaaaatggt 480
gagcaacaat tttatcatta tgccagctct gttaaacctg ctagagttat tttcactgat 540
tcaaaaccag aaattgaatt aggattacaa tcaggtcaat tttggagaaa atttgaagtt 600
tatgaaggtg acaaaaagtt gccaattaaa ttagtatcat acgatactgt taaagattac 660
gcttacattc gcttctctgt ttcaaatgga acaaaagccg ttaaaattgt aagttcaact 720
cacttcaata acaaagaaga aaaatacgat tacacattaa tggaattcgc acaaccaatt 780
tataacagtg cagataaatt caaaactgaa gaagattata aagctgaaaa attattagcg 840
ccatataaaa aagcgaaaac actagaaaga caagtttatg aattaaataa aattcaagat 900
aaacttcctg aaaaattaaa ggctgagtac aagaagaaat tagaggatac aaagaaagct 960
ttagatgagc aagtgaaatc agctattact gaattccaaa atgtacaacc aacaaatgaa 1020
aaaatgactg atttacaaga tacaaaatat gttgtttatg aaagtgttga gaataacgaa 1080
tctatgatgg atactttgt taaacaccct attaaacag gtatgcttaa cggcaaaaaa 1140
tatatggtca tggaaactac taatgacgat tactggaaag atttcatggt tgaaggtcaa 1200
cgtgttagaa ctataagcaa agatgctaaa aataatacta gaacaattat tttcccatat 1260
gttgaaggta aaactctata tgatgctatc gttaaagttc acgtaaaaac gattgattat 1320
gatggacaat accatgtcag aatcgttgat aaagaagcat ttacaaaagc caataccgat 1380
aaatctaaca aaaagaaca acaagataac tcagctaaga aggaagctac tccagctacg 1440
cctagcaaac caacaccatc acctgttgaa aaagaatcac aaaaacaaga cagccaaaaa 1500
gatgacaata aacaattacc aagtgttgaa aaagaaaatg acgcatctag tgagtcaggt 1560
aaagacaaaa cgcctgctac aaaaccaact aaaggtgaag tagaatcaag tagtacaact 1620
ccaactaagg tagtatctac gactcaaaat gttgcaaaac caacaactgc ttcatcaaaa 1680
acaacaaaag atgttgttca aacttcagca ggttctagcg aagcaaaaga tagtgctcca 1740
ttacaaaaag caaacattaa aaacacaaat gatggacaca ctcaaagcca aaacaataaa 1800
aatacacaag aaaataaagc aaaatcatta ccacaaactg gtgaagaatc aaataaagat 1860
atgacattac cattaatggc attactagct ttaagtagca tcgttgcatt cgtattacct 1920
```

```
        agaaaacgta aaaactaa                                          1938

        <210> 54
        <211> 1935
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> cDNA encoding ORF0657n protein of SEQ 5

        <400> 54
        atgaacaaac agcaaaaaga atttaaatca ttttattcaa ttagaaagtc atcactaggc 60
        gttgcatctg tagcgattag tacactttta ttattaatgt caaatggcga agcacaagca 120
        gctgaagaaa caggtggtac aaatacagaa gcacaaccaa aaactgaagc agttgcaagt 180
        ccaacaacaa catctgaaaa agctccagaa actaaaccag tagctaatgc tgtctcagta 240
        tctaataaag aagttgaggc ccctacttct gaaacaaaag aagctaaaga agttaaagaa 300
        gttaaagccc ctaaggaaac aaaaagcagtt aaaccagcaa caaaagccga taacaataca 360
        tatcctattt tgaatcagga acttagagaa gcgattaaaa accctgcaat aaaagataaa 420
        gatcatagcg caccaaactc tcgtccaatt gattttgaaa tgaaaaaaga aaatggtgag 480
        caacaatttt atcattatgc cagctctgtt aaacctgcta gagttatttt cactgattca 540
        aaaccagaaa ttgaattagg attacaatca ggtcaatttt ggagaaaatt tgaagtttat 600
        gagggtgaca aaaagttgcc aattaaatta gtatcatacg atactgttaa agattatgct 660
        tacattcgtt tctctgtatc aaatggaaca aaagctgtta aaattgttag ttcaacacac 720
        ttcaataaca aagaagaaaa atacgattac acattaatgg aattcgcaca accaatttat 780
        aacagtgcag ataaattcaa aactgaagaa gattataaag ctgaaaaatt attagcgcca 840
        tataaaaaag cgaaaacact agaaagacaa gtttatgaat taaataaaat tcaagataaa 900
        cttcctgaaa aattaaaggc tgagtacaag aagaaattag aggatacaaa gaaagcttta 960
        gatgagcaag tgaaatcagc tattactgaa ttccaaaatg tacaaccaac aaatgaaaaa 1020
        atgactgatt tacaagatac aaaatatgtt gtttatgaaa gtgttgagaa taacgaatct 1080
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